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ed Jan 7 09:51:24 2004

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2004, 09:59:31; Search time 21 Seconds (without alignments) 2614.872 Million cell updates/sec

Title: Perfect score: Sequence: US-09-978-194A-132 3108

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

1 MLLSSLVSLAGSVYLAWILF.....PEPEAEPGSCLANISQPTSC 571

283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result

sult No.	Score	Query Match	Length	DB	ID	Description
- !	നം	14.1	1524	إد	T30337	polyprotein - Afri
N	437.5	14.1	343	Н	$\mathbf{r}$	rostasin (EC 3.4
ω	•	٠	1004	N	T30338	in (EC 3.
4.	$\sim$	11.9	790	<b>_</b>	PLPG	(EC 3.
ഗ	10	٠	812	۲	PLMS	(EC 3.4.2
თ	ന	٠	855	N	JC7731	e-bound ar
7	10	11.6	810	<b>-</b>		£
æ	359	•	810	N	I46260	(EC 3.4.2
9	356.5	11.5	812	Ļ	PLBO	(EC 3.4
10	5	11.4	455	N	A61545	1 (EC 3.4.2
11	LJ	•	417	щ	S00845	(EC 3.4.
12	351.5	11.3	810	N	B30848	1 (EC 3.
13	342	11.0	4548	, ,	800657	. –
1 4	ט ט ט	•	1470	۸ د	A3 2 8 6 9	apolipoprocein(a)
7 5	7 7 7 7 7 7 7		200	٦,	ROUTE BOLDED	presilition of the president of the pres
17	این	10.8	270	ν,	\$56160	mast cell tryptase
18	335		275	N	A32410	tase (EC 3.4.
19	333	•	276	N	A38654	ll protei
20	330.5		273	N	A47246	tase (EC 3.
21	330		271	N	A25528	reatic elast
22	329	•	275	N	A35863	e (EC 3.4
23	329	•	275	ผ	B35863	(EC 3.4.
24	328.5		274	N	JC4171	tryptase (EC 3.4.2
25			275	2	C35863	C 3.4.
26	2		366	N	JE0105	testicular serine
27	26		625	_	KFHU1	coagulation factor
28	326.5		638	<b>_</b>	KQMSPL	plasma kallikrein
29	2		263	ب	KYRTB	chymotrypsin (EC 3

밁 5 밁

477 VEYGHGCIYDAVEVYDGAEEKQLIARLCGYTLPLPISSPENTMLIRFKTDMENSYPGFKV 536 303 -----PEMSDEDSCV------417 QFLAIPTKAASACGSAKILKKKGMIYSPNYPDPYPRLKTCSWIIEAPENHIVKLKFEDFN 476 -----RVQGAAFLAQSPET------ 302

312

						317.5										
10.0	10.1	10.1	10.1	10.2	10.2	10.2	10.2	10.3	10.3	10.3	10.4	10.4	10.4	10.5	10.5	
245	421	245	1113	263	761	263	274	271	269	431	269	269	421	416	638	
μ.	N	1	N	N	N	N	N	1	N	N	Ν	N	ш.	μ	1	
КУВОВ	829599	KYBOA	JE0315	A31299	JC5759	A21195	A45754	ELRT2	C26823	S47538	A26823	B26823	S11674	833777	KQRTPL	
chymotrypsin (EC 3	acrosin (EC 3.4.21	chymotrypsin (EC 3	low-density lipopr	chymotrypsin (EC 3	brain-specific ser	chymotrypsin (EC 3	tryptase (EC 3.4.2	pancreatic elastas	pancreatic elastas	acrosin (EC 3.4.21	pancreatic elastas	pancreatic elastas	acrosin (EC 3.4.21	hepsin (EC 3.4.21.	plasma kallikrein	

# ALIGNMENTS

	RESULT 1	
	polyprotein - Afric C;Species: Xenopus C;Date: 22-Oct-1999	- African clawed frog Xenopus laevis (African clawed frog) Oct-1999 #sequence_revision 22-Oct-1999 #text_change 03-Feb-2003
	C;ACCESSION: T3033', R;Yang, J.C.; Lindsay submitted to the EMBL A:Description: CDNA C	; Hedrick, J.L. Jibrary, March 1998 of ovochymase, a chymotrynsin-like protease released from
	A; Description A; Reference n A: Accession:	22.0
,	A;Status: prelimina A;Molecule type: mR	prelimnary; translated from GB/EMBL/DDBJ s type: mRNA
	A; Residues: 1 A; Cross-refer	Residues: 1-1524 YAN> ;Cross-references: EMBL:U81290; NID:q2981640; PID:q2981641; PIDN:AAC24717.1
	C;Superfamily:	tryosin related polyprotein; trypsin homology
	Query Match Best Local Sir Matches 147;	/ Match 14.1%; Score 438.5; DB 2; Length 1524; Local Similarity 18.8%; Pred. No. 9.6e-23; nes 147; Conservative 97; Mismatches 211; Indels 327; Gaps 20;
	Qу 59	GNTVPGEWPWQASVRRQGAHICSGSLVADTWV
	Db 61	GDAAVGGQPWTVSLKLNERHICGGSIVRKDMVVTAAHCVYPVTEIKVSHMTVIVGEYDQQ 120
	Qy 119	GLSPGAEEVGVAALQ-LPRAYNHYSQGSDLAI
	Db 121	VMDSQEQSIPVSHIEPHPNYRGDGNMGYDIALVFLSKPIIFGSQVQPICLPQVGEKIEAG 180
	Qy 174	ASCWATGWDQDTSDAPGTLRNLRLR
	Db 181	TLCVSSGWGRLEENGDLSPVLQE
	Оу 232	PGVQGPCQGDSGGPVLCLEPDGHWVQAGIIS
	Db 237	EGGMDACQGDSGGPFVCRRRSGVWFLAGCVSWGLGCGRSWGAKQIIRSQSGSPAIFSRVS 296
	Оу 279	TAAHSS 288
	Db 297	SVLDFLRPPKLTGGCSSKGRTITGKNGTVRYPLSGNYSINSVCRWMLAVQKAKTIEIRFL 356
	Оу 289	288
	Db 357	QLDIEDHATCTFDYLSFTVNEKMIRKVCGSTIPSPLIVRSNKVTVTFFSDGTFTGRGFEI 416
	Оу 289	RVQGAAFLAQSPET 302
	,	

283 287	O; Conservative 48 PQGKAKRHGNTVPGEWPWQA     :     :           PQARITGGSSAVAGQWPWQV	
Qy 235 QGPCQCDSGGPVLCLEPDGH :       :   Db 227 KDACQGDSGGPLLCQRRHGS	atch 14.1%; Score 437.5; DB 1; Length 343; cal Similarity 35.3%; Pred. No. 2.1e-23;	
177 171	F;323-341/Domain: transmembrane #status predicted <tmm1> F;37-154,70-86,168-244,201-223,334-262/Disulfide bonds: #status predicted F;85,134,238,Acctive site: His, Asp. Ser #status predicted F;85,134,238,Acctive site: His, Asp. Ser #status predicted F;159/Binding site: carbohydrate (Asn) (covalent) #status experimental</tmm1>	
Qy 123 GABEVGVAALQLPRAYNH   : : :     Db 111 ETEQMFRVIEIFKHPNFNQS	F;33-44,45-343/Product: prostasin #status predicted <mat> F;33-44/Domain: prostasin light chain #status predicted <chl> F;45-343/Domain: prostasin heavy chain #status predicted <chh> F;45-281/Domain: trypsin homology <try></try></chh></chl></mat>	
Qy 64 GEWPWOASVRROGAHICSGS   :     :	A;Map position: 16p11.2-16p11.2 C;Superfamily: trypsin; trypsin homology C;Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein F;1-32/Domain: signal sequence #status predicted <sig></sig>	
Query Match Best Local Similarity 19.3%; Matches 155; Conservative 92	A;Residues: 45-64 <yua> C;Genetics: A;Gene: GDB:PRSS8 A;Cross-references: GDB:676446; OMIM:600823</yua>	
A; Residues: 46-73 < HAR> C; Comment: This protease is found: C; Superfamily: oviductin; trypsin! C; Keywords: extracellular protein;	J. Biol. Chem. 269, 18843-18848, 1994 A;Title: Prostasin is a novel human serine proteinase from seminal fluid. Purification, A;Reference number: A54866; MUID:94308140; PMID:8034638 A;Accession: A54866 A;Molecule type: protein	
A; TITLE: OVIGUETIN. FURTILICATION at A; Reference number: A40242; MUID:9 A; Accession: A40242 A; Molecule type: protein	A; Experimental source: prostate A; Note: parts of this sequence were determined by protein sequencing R;Yu, J.X.; Chao, L.; Chao, J.	
A;Cross-references: EMBL:U81291; N R;Hardy, D.M.; Hedrick, J.L. Biochemistry 31, 4466-4472, 1992		
A; Status: preliminary; translated A; Status: preliminary; translated A; Molecule type: mRNA A; Residues: 1-1004 <lin></lin>	A;Title: Molecular cloning, tissue-specific expression, and cellular localization of hum A;Reference number: A57014; MUID:95286644; PMID:7768952 A;Accession: A57014	
enc enc epr	C;Species: nome sapiens (man) C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 21-Apr-2003 C;Accession: A57014; A54866 C;Accession: A57014; Chao, I.; C	
1 0 0 0 C	RESULT 2 AS7014 , prostasin (EC 3.4.21) precursor - human	
RESULI 3 T30338 oviductin (EC 3.4.21) - African	· Db 813 QN 814	
	Qy 540 SS 541	
Qy 319 TAGPOAGAPSPW 330	Qy 490PSCEGLSGAPLVHEVRGTWF-LAGLHSFGDACQGPARPAVFTALPAYEDWV 539	
Db 274 ASSYASWIQSKVTELQPRVV	Db 716 EDGQPALGLQQLQLPILDSIICNTSYYSGELTDHMLC 752	
Qy 279 TAAHSSWLQARVQGAAFI	SSLQTVPVTLLGPRACSRLHAAPGGDGSF	
Qy 219 NPARPGMLCGGPQPGVQGPC :         :   Db 215 HFVQEDMVCAGYVEGGKDAC	Qy 384 KQLILHGAYTHÞEGGYDMALLLLAQPVTLGASLRÞLCLÞYPDHHLÞDGERGWVL 437   :	•
155		
163	32 WEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGL 3	
Qy	QY 313	

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clawed frog)
n clawed frog)
ision 22-Oct-1999 #text_change 03-Feb-2003
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                                                                                                                                                                                                EVYĹPIVDLSSCLHVMSAĹKGTVVŚS----YIVCAGFPEGG 226
                                                                                                                                                                                                                                               NLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGV 234
                                                                                                                                                                                                                                                                                                    SQPMNYDVAVLLLDGSVTFDENIQPACLPNPDDVFEPGDLC 170
                                                                                                                                                                                                                                                                                                                                                                                                                                   SLVADTWVLTAAHC-FEKAAATELNSWSVVLGSLQREGLSP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 384.5; DB 2; Length 1004; Pred. No. 3.7e-19; 2; Mismatches 232; Indels 325; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in oviductal secretory granules and is secreted to prov
homology
; hydrolase; serine proteinase
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al CUB domains.
99184825, PMID:10084976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLAQSPETPEMSDEDSCVACGS------LR----- 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTN 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHVAPSVSLLTPKPLQQLEVPLISRETCNCLYNIDAKPEEP 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DQDTSD----APGTLRNLRLRLISRPTCNCIYNQLHQRHLS 218
SMQDGVLSGKSGELIFLKNPMSVTRTMSGAPGFSLSLKTC 346
                                                                                                                                                                                                                                                                                                                                                     HYSQGSDLALLQLAHPTTH----TPLCLPQPAHRFPFGASC 176
                                                                                                                                                                                                                                                                                                                                                                                                       TLVSHCHVLTAAHCLLDRNVKLYMR----VYIGEYD-QILKE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VID:g1754713; PID:g1754714; PIDN:AAB53972.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hedrick, J.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from GB/EMBL/DDBJ
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A;Accession: A;Andecule type: protein
A;Molecule type: protein
A;Residues: 1-57 < dBRU's
A;Residues: 1-57 < dBRU's
R;Marti, T.; Schaller, J.; Rickli, E.E.
Eur. J. Biochem. 149, 279-285, 1985
Eur. J. Biochem. 149, 279-285, 1985
A;Title: Determination of the complete amino-acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-560 <SCH>
A;Residues: 1-560 <SCH>
R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.,
Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,
A;Reference number: S03735; MUID:81212097; PMID:7238497
A;Accession: S03737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Sus scrofa domestica (domestic pig)
C;Date: 07-Sep-1990 #sequence revision 01-Nov-1996 #text_change 18-Jul-1997
C;Accession: S03737; A25834
R;Schaller, J; Marti, T; Roesselet, S.J.; Kaempfer, U.; Rickli, E.E.
Fibrinolysis 1, 91-102, 1987
A;Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison A;Reference number: S03733
A;Accession: S03733
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A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine prote
F;1-790/Product: plasminogen #status predicted <PRO>
                                                                                                                                                          A;Reference number: A25834;
A;Accession: A25834
A;Molecule type: protein
A;Residues: 450-790 <MAR>
C;Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N; Alternate names: plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasmin (EC 3.4.21.7) precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEEAVPHSWPWHTSLQYAGEHVCDGAIIAENWILTTASCVLNRKFNDVWLVDPGIHDLLR 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERDNDKGFRATFTFVSPNSLVEDSRQGNMPSTNKKETTAQDSICGVSQVPPIFIYNSIAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENRTGFVLYYSAVEPNTYPDSGCGSFAVLFEEGEIQSMNYPENYLSNSRCHWIIHGPSGS 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSCLNFTHLDIESDFACNLDYLAIYTDSHRLIGKFCGDIPPRSLLISFSSIKLNFFSDFH 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QDNDSCSEQSGSPLVCLLEKKGIYTIFGIASWGVNCKENSKPGIYTKVSPFIDWIRQI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --RGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAA-PGGDGSPILPGMVCTSAVG-- 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGHNQKGLVKQIIPHPSFSSQTNDFDIALVELDESLQFNSDIFPICLPGKTSELAPASLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P--EEWGL-KQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------MSDTGQIHSNLGDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -ELPSCEGLSGAPLV--HEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVSSLDW 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---PWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEEWSVGLG----TR 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -MSDEDSC--
                                                                                                           fibrin of blood clots; acts as a proteolytic factor in a follicle; also activates the urokinase-type plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -SLRTAGPQAGAPS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OSPETPE---
                                                                                                                                                                                                                                                                               porcine miniplasminogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        818
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F;1-77/Domain: plasminogen-related protein precursor homology (fragment)
F;1-77/Domain: activation peptide #status predicted <APT>
F;1-560/Product: plasmin chain A #status predicted <ACH>
F;84-162/Domain: kringle homology <KR1>
F;166-43/Domain: kringle homology <KR2>
F;256-333/Domain: kringle homology <KR3>
F;256-333/Domain: kringle homology <KR4>
F;358-435/Domain: kringle homology <KR4>
F;450-790/Product: miniplasminogen #status experimental <MIN>
F;461-540/Domain: kringle homology <KR5>
F;461-790/Product: plasmin chain B #status experimental <BCH>
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F;30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,305-
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plasmin (EC 3.4.21.7) precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #status predicted
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                                                                                                                                                                                                                 693
                                                                                                                                                                                                                                                                                                                                                                                                       581
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                                                                                                                                                                                                                                                             189
                                                                                                                                                                                                                                                                                                                                                                                                                                                   74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 LYDFCIV--CITTYAINVSLMWLSF----RKVQEPQGKAKRHGN--TVPGEWPWQASVR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LFDYCDVPQCVTS--
                                                                                                                                                                                                                                                                                                                                                       LPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGWDQDTSD-A 188
                                                                                                                                                                                                                                                                                                                                                                                                     RYRGHFCGGTLISPEWVLTAKHCLEKSSSP--SSYKVILGAHEEYHLGEGVQEIDVSKL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQ 133
                                                                                                                                                                   LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 287
                                                                                                                                                                                                                 AGLLKEARLPVIENKVCN-----RYEYLGGKVSPNELCAGHLAGGIDSCQGDSGGPLVC
                                                                                                                                                                                                                                                          PGTLRNLRLRSRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLC 248
                                                                                                                    FEKDKYILQ-GVTSWGLGCALPNKPGVYVRVSRFVTWIE
                                                                                                                                                                                                                                                                                                           ----FKEPSE-ADIALLKLSSPAVITDKVIPACLPTPNYVVADRTACYITGWGETKGTYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.9%;
32.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 370.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SFDCGKPKVEPKKCPARVVGGCVSIPHSWPWQISLRY
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                                                                                                                    784
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                                                                                                                                                                                                                                                                                                             692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
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A;Molecule type: protein
A;Residues: 22-27 <LI2>
C;Comment: Plasminogen is synthesized by the kidney and is present in plasma a: C;Comment: Plasminogen is converted into plasmin by plasminogen activators, borediately after dissociation from the clot. In the presence of the inhibitor, is einhibitor, the activation involves also removal of the activation peptide. C;Comment: Stromelysin I (see PIR:KCMSSI) acts on plasminogen to produce angion eful in treating solid tumors.
C;Function:
C;Function: dissolves the fibrin of blood clots; acts as a proteolytic fact. C;Accession: A38514; S48202; S48203
R;Degen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.
Genomics B, 49-61, 1990
A;Title: Characterization of the cDNA coding for mouse plasminogen and localization A;Reference number: A38514; MUID:91184812; PMID:2081600
A;Accession: A38514 A;Cross-references: GB:J04766; NID:g200402; PIDN:AAA50168.1; R;Lijnen, H:R.; van Hoef, B.; Beelen, V.; Collen, D. Eur. J. Biochem. 224, 863-871, 1994
A;Title: Characterization of the murine plasma fibrinolytic sA;Reference number: S48202; MUID:95010076; PMID:7523120 N;Contains: angiostatin; plasminogen C;Species: Mus musculus (house mouse) C;Date: 20-Sep-1991 #sequence\_revision 01-Nov-1996 #text\_change 18-Jun-1999 C;Accession: A38514; S48202; S48203 A; Molecule type: protein A; Residues: 20-25 <LIJ>A; Accession: S48203 A; Reference number: S48202; A; Accession: S48202 A; Molecule type: mRNA A; Residues: 1-812 < DEG> PID:g200403

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RiKishi, K.; Yamazaki, K.; Yasuda, I.; Yahagi, N.; Ichinose, M.; Tsuchiya, Y.; J. Biochem. 130, 425-430, 2001
A;Title: Characterization of a membrane-bound arginine-specific serine protease A;Reference number: JC7731; MUID:21421307; PMID:11530019
A;Accession: JC7731
A;Experimental source: strain Male, 7-week-old
R;Satomi, S.; Yamasaki, Y.; Tsuzuki, S.; Hitomi, Y.; Iwanaga, T.; Fushiki, T.
Biochem. Biophys. Res. Commun. 287, 995-1002, 2001
A;Title: A role for membrane-type serine protease (MT-SP1) in intestinal epithelial A;Reference number: JC7775; PMID:11573963
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F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR2>
                                                                                                                                                                                                                   A; Residues: 1-855 < KIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                   membrane-bound arginine-specific serine proteinase precursor - C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_changeC;Accession: JC7731; JC7775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
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F;377-454/Domain: kringle homology <KR4>
F;377-454/Domain: kringle homology <KR5>
F;481-560/Domain: kringle homology <KR5>
F;582-812/Domain: chain B #status predicted <BCH>
F;582-812/Domain: trypsin homology <TRY
F;582-805/Domain: trypsin homology <TRY
F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;136,308/Binding site: carbohydrate (Asn) (covalent) #status predicted;466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted;581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental
                                                                                                                                                                                      Cross-references: DDBJ:AB049189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;20-812/Product: plasminogen #status predicted <PRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: plasmin; kringle homology; plasminogen-related protein; Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      624,667,762/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 -- GAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 LYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKR-HGNTV-----PGEWPWQASVRRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CFEKDKYILQ-GVTSWGLGCARPNKPGVYVRVSRFVDWIEREMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYDYCDIPLCASA-----SSFECGKPQVEPKKCPGRVVGGCVANPHSWPWQISLRTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               #text_change 03-Feb-2003
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A,Molecule type: DNA
A,Residues: 1-810 <-PET>
A,Cross-references: GB:J05286; GB:M34276; NID:g190064; PIDN:AAA60113.1; PID:g387026
A,Cross-references: GB:J05286; GB:M34276; NID:g190064; PIDN:AAA60113.1; PID:g387026
A,Experimental source: leukocyte; lung fibroblast
R;Malgaretti, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S
Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990
A;Title: Definition of the transcription initiation site of human plasminogen gene: A;Reference number: 152242; MUID:91097523; PMID:2268308
A;Accession: 152242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Contains: angiostatin; microplasmin; plasminogen
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Dec-1994 #text_change 15-Sep-2000
C;Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627;
R;Petersen, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.
J. Biol. Chem. 265, 6104-611, 1990
A;Title: Characterization of the gene for human plasminogen, a key proenzyme
A;Reference number: A35229; MUID:90202879; PMID:2318848
A;Accession: A35229
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A;Cross-references: DDBJ-RB037898
C;Comment: This enzyme, an epithelial-derived, type II integral membrane serine prote of specific proteins or peptides on the brushborder membranes. It also participates lial migration and/or cell loss.
  A;Experimental source: R;Malinowski, D.P.; Sa
                                                 A;Residues: 1-471,'D',473-810 <FOR>
A;Cross-references: GB:X05199; NID:g35530; PIDN:CAA28831.1;
                                                                               A; Molecule type: mRNA
A; Residues: 1-471, 'D'
                                                                                                                                                        A; Title: Molecular cloning and characterization of a fu A; Reference number: A26646; MUID:87162490; PMID:3030813
                                                                                                                                                                                                         A;Cross-references: GB:M62890; NID:g190092; PIDN:AAA36454.1; PID:g553613 R;Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O. FEBS Lett. 213, 254-260, 1987
                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-16 < MALL>
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C;Keywords: protein digestion
                                                                                                                                   A; Accession: A26646
                                                                                                                                                                                                                                                                                                                                             A;Status: translated from GB/EMBL/DDBJ
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D.P.; Sadler, J.
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    J. Biol. Chem. 271, 29461-29467, 1996
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A;Contents: annotation
R;Lijnen. H P. 172----
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A;Accession: A04627
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R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M. Bur. J. Biochem. 114, 445-470, 1981
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A;Title: Studies on the active center of human plasmin. Parti. A;Reference number: A92048; MUID:69234739; PMID:4240117
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A; Residues: 20-71,'E',73-85,87-106,'D',108-360,'E',362-810 <SOT>
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A; Accession: A00929
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                                                                                                                                                                                                                                                                                                                                                           R;Vali, Z.; Patthy, L.
R;Vali, Z.; Patthy, L.
Riol. Chem. 259, 13690-13694,
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A;Residues: 483-507, 'E', 509-604 <WI3>
A;Residues: K.C.; Bernabe, P.; Arzadon, L.; Summaria,
R;Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria,
J. Biol. Chem. 248, 1631-1633, 1973
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A;Reference number: A92125; MUID:73149248; PMID:46947
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J. Biochem.
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A; Residues: 367-419
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                                                                                                              Biol. Chem. 259, 13690-13694, 1984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen; Reference number: A04626; MUID:76043692; PMID:126863; Accession: A04626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Molecule type: mRNA;Residues: 292-471,'D',473-810 <MAL2>;Cross-references: GB:K02922; NID:g190112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Title: Characterization of a complementary deoxyribonucleic;Reference number: I45961; MUID:85023311; PMID:6148961;Accession: I62738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Residues: 20-50,'Q',51-71,'E',73-85,87-100 <WI2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: translated from GB/EMBL/DDBJ
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PMID:4694729
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rg-580, resulting in two chains connected by two
C;Comment: Microplasmin is formed by autolytic cl
C;Comment: Stromelysin 1 (see PIR:KCHUS1) acts on
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submitted to the Brookhaven Protein Data Bank, August 1996
A;Reference number: A65803; PDB:1HPJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Contents: annotation; X-ray crystallography, R;Stec, B.; Teeter, M.M.; Whitlow, M.; Yamano, submitted to the Brookhaven Protein Data Bank, A;Reference number: A65980; PDB:IKRN
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R;Co Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.;
Biochemistry 31, 270-279, 1992
A;Title: Crystal structure of the kringle 2 domain of tissue
A;Reference number: A39483; MUID:92118803; PMID:1310033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M. Blochemistry 30, 10589-10594, 1991
A;Title: The refined structure of the epsilon-aminocaproic acid complex of A;Reference number: A58818; MUID:92031503; PMID:1657149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochemistry 37, 4699-4702, 1998
A;Title: Generation of an angiostatin-like fragment from plasminogen by
A;Reference number: A58812; MUID:9548733; PMID:9548733
                                                                                                                                          C;Comment: Plasminogen C;Comment: Plasminogen
                                                                                                                                                                                                                          Eur. J. Biochem. 221, 939-949, 1994
A;Title: Solution structure of the epsilon-aminohexanoic A;Reference number: A58817; MUID:94237158; PMID:8181476
                                                                                                                                                                                                                                                                                                                                        A;Title: (1)H-NMR assignments and secondary structure of human plasminogen A;Reference number: S43645; MUID:94237157; PMID:8181475
A;Contents: annotation; conformation by (1)H-NMR, residues 96-184
                                                                                                                                                                                                                                                                                                                                                                                                                             R;Rejante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 927-937, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G.
Biochemistry 30, 10576-10588, 1991
A;Title: Crystal and molecular structure of human plasminogen
A;Reference number: A58819; MUID:92031502; PMID:1657148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the Brookhaven Protein Data Bank, December 1995 A;Reference number: A65245; PDB:LCEB
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A;Contents: annotation; X-ray crystallography,
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                                                                                     C; Comment: Plasmin
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R:Rejante, M.; Llinas, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the Brookhaven Protein Data Bank,
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                                                                                                                                       annotation; conformation by (1)H-NMR
Plasminogen is synthesized by the kidney and is present in plasma
Plasminogen is converted to plasmin by plasminogen activators (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              annotation
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                                                                                     is inactivated by alpha-2-antiplasmin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conformation by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (1)H-NMR, residues 103-181
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PMID:1310033
wo disulfide bonds. Without the inhibitor, cleavage of plasmin under artificial condi on plasminogen to produce angiostatin. Tog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          April 1994
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e PIR:UKHU ar
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A;Cross-references: EMBL:U33171; NID:g1046360; PID:g1046361
C;Superfamily: plasmin; kringle homology; plasminogen-relat
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;97-580,581-810/Product: plasmin #status experimental <MAT: F;97-580/Domain: plasmin chain A #status experimental <CHA> F;97-580/Domain: kringle homology <KR1> F;103-181/Domain: kringle homology <KR2> F;185-262/Domain: kringle homology <KR3> F;275-352/Domain: kringle homology <KR3> F;377-454/Domain: kringle homology <KR4> F;481-560/Domain: kringle homology <KR4>
                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-810 <LAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasmin (EC 3.4.21.7) precursor - western European hedgehog
C;Species: Erinaceus europaeus (western European hedgehog)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Pathway: fibrinolysis C; Superfamily: ----
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A; Introns: 17/1; 62/2; 98
C; Function:
                                                   F;275-352/Domain:
                                                                       F;185-262/Domain:
                                                                                                                                                                                                                                                                                                   A; Accession: 146260
                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 270, 24004-24009, 1995
A; Title: The recurring evolution of Lp(a):
A; Reference number: I46259; MUID:96025778;
                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: I46260
R;Lawn, R.M.; Boonmark,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology; Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydr; 1-96/Domain: plasminogen-related protein precursor homology <PLPH>
;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                 ;1-96/Domain: plasminogen-related protein precursor homology;1-96/Domain: kringle homology <KR1>
                                                                                                                                                    Superfamily: plasmin; kringle homology; plasminogen-related; Keywords: hydrolase; serine proteinase
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           550-580,581-810/Product: microplasmin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-96/Domain: activation peptide #status experimental <APT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-810/Product: plasminogen #status experimental <PRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: GDB:119498; OMIM:173350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene: GDB:PLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              551 LYDYCDVPQCAAP-----SF-DCGKPQVEPKKCPGRVVGGCVAHPHSWPWQVSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <del>(</del>ک
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGW--DQDTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRFGMHFCGGTLISPEWVLTAAHCLEKSPRP--SSYKVILGAHQEVNLEPHVQEIEVSRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -ROGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLOREGLSPGAEEVGVAAL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYDECIV--CITTYAINVSLMWLSERKVQEPQGKAKR-HGNTV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VCFEKDKYILQ-GVTSWGLGCARPNKPGVYVRVSRFVTWIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GA-GLLKEAQLPVIENKVCN-----RYEFLNGRVQSTELCAGHLAGGTDSCQGDSGGPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DAPGTLRNLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLE----PTRKDIALLKLSSPAVITDKVIPACLPSPNYVVADRTECFITGWGETQGTF
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kringle homology
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homology
homology
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33.8%; Pred. No. 1.6e
tive 39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fibrin of blood clots; acts as a proteolytic factor in a follicle; also activates the urokinase-type plasminogen a
                                                                                                                                                                                                                                                                                                                                                                                               Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne,
                            <KR3>
     <KR5>
                                                                               <KR2>
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                                                                                                                                                                                                                                                                                                                             Insights from PMID:7592597
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                                                                                                                                                                           precursor homology
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                                                                                                    194
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                                                                                                                                                                                                                                                                                                                                                         Similarity
YILQ-GVTSWGLGCARLTRPGVYVRVSRYVSWLQ 804
                               HWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ
                                                                                                 NLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLCLEPDG
                                                                                                                                  R----ADIALLKLSSPAIITDKDHPACLPNSNYMVADRSLCYITGWGETKGTYGAGLLK
                                                                                                                                                                                                       FCGGTLISPEWVVTAAHCLEKFSNPAI--YKVVLGAHQETRLERDVQIKGVTKMFL-EPY
                                                                                                                                                                                                                                     ICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQLPRAY
                                                                                                                                                                                                                                                                        LFDYCDIPHCVSPSSADCG------KPKVEPKKCPGRVGGCVAHPHSWPWQVSLRRFGQH
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                                                                                                                                                                    NHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGWDQDTSD-APGTLR
                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                         11.6%;
                                                                                                                                                                                                                                                                                                                                         42; Mismatches 112;
                                                                 -ROSFLNGRVRSTELCAGHLAGGVDSCQGDSGGPLVCFEKDR
                                                                                                                                                                                                                                                                                                                                                         Score 359; DB 2; Pred. No. 1.8e-17;
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A;Molecule type: mRNA
A;Rosidues: 706-743,", 745-812 <MAL>
A;Residues: 706-743,", 745-812 <MAL>
A;Residues: 706-763,", 745-812 <MAL>
A;Residues: Toferences: GB:K02915; NID:g163551; PIDN:AAA30714.1; PID:g163552
A;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, Eur. J. Biochem. 114, 465-470, 1981
Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of huma A;Reference number: S03735; MUID:81212097; PMID:7238497
A;Accession: S03736
                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 27-334, 'D', 336-515, 'H', 517-554, 'L', 556-812 <SCH>
R; Malinowski, D.P.; Sadlar, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A; Title: Characterization of a complementary deoxyribonucleic A; Reference number: I45961, MUDI: 85023311; PMID: 6148961
A; Accession: I45961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Berglund, L.; Andersen, M.D.; Petersen, T. submitted to the EMBL Data Library, May 1994 A;Description: Cloning and characterizatin o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Complete amino acid sequence of bovine plasminogen. A;Reference number: A25835; MUID:85203906; PMID:3846532 A;Accession: A25835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Note: it is uncertain whether Met-1 or Met-8
R;Schaller, J.; Moser, P.W.; Dannegger-Muller,
Eur. J. Biochem. 149, 267-278, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: Cloning and A; Reference number: $45046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1987 #sequence revision 28-Apr-1995
C;Accession: S45046; A25835; T45961; S03736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasmin (EC 3.4.21.7) precursor -
N;Alternate names: plasminogen
                                                                                                                                                                                                                                                                                  A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X79402; NID:g494962; PIDN:CAA55939.1; A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-812 <BER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S45046
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                                                                                                                                                                                                                                                                                                                                                                                 acid coding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S.J.; Kampfer,
                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                     human
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A;Pathway: fibrinolysis C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology: C;Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma;

fibrin of blood clots; acts as a proteolytic factor in follicle; also activates the urokinase-type plasminoger

plasminogen

a vai

of human,

3

ns the walls of the graafian A; Description: dissolves the A; Molecule type: protein A; Residues: 27-83 < BRU>

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N;Contains: miniplasminogen
C;Species: Equus caballus (domestic horse
C;Date: 28-Oct-1994 #sequence_revision 01
C;Accession: A61545; S17527
R;Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
A;Title: Structural aspects of the plasmi
A;Reference number: A61545; MUID:89005015
A;Accession: A61545
        A;Molecule type: protein
A;Residues: 118-455 <SC2>
A;Residues: 118-455 <SC2>
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precur
C;Superfamily: plasmin; kringle homology; plasminogen-related protein periode
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine p
F;1-33,Jomain: activation peptide (fragment) #status experimental APT'>
F;34-117,118-225,226-455/Product: plasmin (fragments) #status experimental <
F;37-114/Domain: kringle homology <KR4>
F;37-114/Domain: kringle homology <KR4>
F;37-114/Domain: kringle homology <KR4>
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                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 1-33,34-117 <SCH>
R;Residues: 1-35,54-117 <SCH>
R;Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.
Protein Seq. Data Anal. 4, 69-74, 1991
A;Title: Complete amino acid sequence of equine miniplasminogen.
A;Reference number: S17527; MUID:92052077; PMID:1946332
A;Accession: S17527
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F;192-269/Domain: kringle homology <KR2>
F;282-359/Domain: kringle homology <KR3>
F;284-461/Domain: kringle homology <KR4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names: plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasmin (EC 3.4.21.7) precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;485-564/Domain: kringle homology <KR5>
F;584-812/Domain: plasmin chain B #status experimental <BCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;584-805/Domain: Erypsin homology <TRY>
;56-80,60-68,110-188,131-171,159-183,192-269,195-323,213-252,241-264,282-359,303-342,33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-812/Product:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 HYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGWDQDTSD-APGTLRN 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
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| 84; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YDFCIV--CITTYAINVSLMWLSFRKVQEPQGKAKRHGNTV--PGEWPWQASVRRQGAHI 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FDYCDVPQCESSFDCGKP-----KVEPKKCSGRIVGGCVSKPHSWPWQVSLRRSSRHF
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miniplasminogen #status experimental <MIN>
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Pred. No. 2.7e-17;
6; Mismatches 112
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                                             experimental <MAT:
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                                                                                                      <PRO>
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A;Cross-references: GDB:135685; OMIM:142440
A;Map position: 19q11-19q13.2
C;Superfamily: hepsin; trypsin homology
C;Keywords: hydrolase; liver; serine proteinase; transmembrane
E;23-45/Domain: transmembrane #scatus predicted <TMN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hepsin (EC 3.4.21:-) - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec_1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1999
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S00845
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F;226-455/Domain: plasmin chain B #status experimental <BCF
F;226-448/Domain: trypsin homology <TRY>
F;267,310,405/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                             F;163-400/Domain: trypsin homology <TRY>
F;188-204,291-359,322-338,349-381/Disulfide bonds: #status
F;203,257,353/Active site: His, Asp, Ser #status predicted
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A; Residues: 1-417 < LEY >
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A;Title: A novel trypsin-like serine protease (hepsin) with A;Reference number: S00845; MUID:88209431; PMID:2835076
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                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                         120
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                     GG-PQPGVQGPCQGDSGGPVLC---LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHS
                                                          LVDGKICTVTGWGNTQYYGQQAGVLQEARVPIISNDVCN-----GADFYGNQIKPKMFC
                                                                                                                                                                         LSPGAEEVGVAAL-----QLP-RAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHR
                                                                                                                                                                                                                                    NTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREG
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                                                                                               FPFGASCWATGW--DQDTSDAPGTLRNLRLISRPTCNCIYNQLHQRHLSNPARPGMLC
                                                                                                                                    ASPHGLQLGVQAVVYHGGYLPFRDPNSEENSNDIALVHLSSPLPLTEYIQPVCLPAAGQA
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plasmin chain B #status experimental <BCH>
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31.5%;
   11.4%; Score 353; DB 1; 35.0%; Pred. No. 2.2e-17;
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Pred. No. 1.6e-17
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text_change 08-Dec-2000
C;Accession: $00657; A28017; A47277; I60906; A47233; I52415; I65286
R;McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Eaton, D.L.; Chen, E.Y.; Fless, (Nature 330, 132-137, 1987
Nature 330, 132-137, 1987
A;Title: cDNA sequence of human apolipoprotein(a) is homologous to plasminogen
A;Reference number: $00657; MUID:88039109; PMID:3670400
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F;185-562/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR5>
F;481-560/Domain: kringle homology <KR5>
F;581-803/Domain: krypgin homology <TKY>
F;4973,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,3:
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                                                                                                                                                                                           apoprotein(a) (EC 3.4.21.-) precursor [validated] - human
N;Alternate names: apolipoprotein(a); lipoprotein(a) chain apo(a)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: plasmin; kringle homology; plasminogen-related protein precurse; keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase; legycoprotein; precursor homology <PLPH>
[1-9/Domain: plasminogen-related protein precursor homology <PLPH>
[1-9/Domain: signal sequence #status predicted <SIG>
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Macaca
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                                                                                                                                                                                                                                                                                                                                                                                           PVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 287
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32.5%;
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Pred. No. 5.9e-17;
5; Mismatches 99
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A;Cross-references: GB:LO7899; NID:g967973; PID:g967974 R;Malgaretti, N.; Acquati, F.; Magnaghi, P.; Bruno, L.; Frcc. Natl. Acad. Sci. U.S.A. 89, 11584-11588, 1992 A;Title: Characterization by yeast artificial chromosome A;Reference number: A47233; MUID:93087573; PMID:1454851 A;Accession: I60906
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A;Cross-references: GB:X06290; EMBL:X06696; NID:g28619; PIDN:CAA29618.1; PID:g28620
A;Cross-references: GB:X06290; EMBL:X06696; NID:g28619; PIDN:CAA29618.1; PID:g28620
R;Eaton, D.L.; Fless, G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lawn, R.M.;
Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987
A;Title: Partial amino acid sequence of apolipoprotein(a) shows that it is homologous to A;Reference number: A28017; MUID:87204109; PMID:3472206
A;Accession: A28017
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F;1054-1131/Domain: kringle
F;1168-1245/Domain: kringle
F;1282-1359/Domain: kringle
                                                                                        F,256-333/Domain: kringle homology <KR3>
F,370-47/Domain: kringle homology <KR4>
F,484-561/Domain: kringle homology <KR5>
F,598-675/Domain: kringle homology <KR6>
F,712-789/Domain: kringle homology <KR7>
F,712-798/Domain: kringle homology <KR8>
F,826-903/Domain: kringle homology <KR8>
                                                                                                                                                                                                                                                                                                                                                                                C;Keywords: hydrolase; kringle; lipid binding; lipoprotein; F;1-19/Domain: signal sequence #status predicted <SIG> F;20-4548/Product: apolipoprotein(a) #status experimental <N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochemistry 31, 3113-3118, 1992
A;Title: Multiple members of the plasminogen-apolipoprotein(a)
A;Reference number: IS2415; MUID:92207924; PMID:1554698
A;Accession: I52415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rs of kringle repeats
C;Superfamily: apolipoprotein(a); kringle homology; trypsin homology
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A; Note: several genes closely linked on chromosome
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A; Residues: 1-16 < RE4 >
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A; Residues: 1-16 < RE5 >
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A; Residues: 1-16 < RE2 >
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A;Residues: 20-21,'P',23-34;177-179,'N',181-186,'T',188-196,'DKG',200;292-314,'W',316-31
                                                                                                                                                                                                                                                                                                                     F;142-219/Domain: kring
                                                                                                                                                                                                                                                                                                                                                         F;28-105/Domain: kringle homology <KRl>
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A; Residues: 1-16 < RE3>
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homology <KR11 >
homology <KR12 >
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apolipoprotein(a) (EC 3.4.21.-) - rhesus macaque (fragment) C;Species: Macaca mulatta (rhesus macaque) C;Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change C;Accession: A32869; A30848 R;Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989 A;Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, A;Reference number: A32869; MUID:89174660; PMID:2923643 A;Accession: A32869.
                A;Molecule type: mRNA
A;Residues: 1-1420 <TON>
A;Residues: 1-1420 <TON>
A;Residues: 1-1420 <TON>
A;Cross-references: GB:J04635; NID:g342072; PIDN:AAA36833.1; PID:g342073
C;Superfamily: apolipoprotein(a); kringle homology; trypsin homology
C;Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine protei
F;50-127/Domain: kringle homology <KR1>
F;164-241/Domain: kringle homology <KR3>
F;278-355/Domain: kringle homology <KR3>
F;392-469/Domain: kringle homology <KR4>
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C;Superfamily; plasmin; kringle homology; plasminogen-related protein precursor homology; c;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase; z; F;1-37,38-117,118-460/Product: plasminogen (fragments) #status experimental <PRO> F;1-37/Domain: activation peptide (fragment) #status experimental <APT> F;38-117,118-230,231-460/Product: plasmin (fragments) #status experimental <MAT> F;41-118/Domain: kringle homology <KR4> F;118-460/Product: miniplasminogen #status experimental <MIN> F;118-460/Product: miniplasminogen #status experimental <MIN> F;126-460/Domain: kringle homology <KR5> F;236-460/Domain: plasmin chain B #status experimental <BCH> F;231-453/Domain: trypsin homology <TRY> F;231-453/Domain: trypsin homology <TRY> F;272,315,410/Active site: His, Asp, Ser #status predicted
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A; Residues: 1-37;38-117 <SCH>
R; Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.
Protein Seq. Data Anal. 5, 21-25, 1992
A; Title: Complete amino acid sequence of ovine miniplasminogen.
A; Reference number: S28200; MUID:93149995; PMID:1492092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Ovis orientalis aries, Ovis ammon aries C;Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 C;Accession: B61545; S28200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasmin (EC 3.4.21.7) precursor
N;Alternate names: plasminogen
N;Contains: miniplasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;1068-1145/Domain: kringle homology <KR10>F;1191-1413/Domain: trypsin homology <TRY>
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F;726-603/Domain: kringle homology <KR7>
F;840-917/Domain: kringle homology <KR8>
F;954-1031/Domain: kringle homology <KR9>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Structural aspects of the plasminogen of various A; Reference number: A61545; MUID:89005015; PMID:3168975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 118-460 <SC2>
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                                                                                                                 47;
                                                                                                              Score 338; DB 2;
Pred. No. 2.8e-16;
17; Mismatches 114
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#text_change 17-Mar-1999
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Search	Db ·	Ş	Ф	γQ	Дb	Ş	Вb	Ş
Search completed: January 6, 2004, 10:03:10	421 KYILQ-GVTSWGLGCARPNKPGVYVRVSTYVPWIE 454	253 GHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 287	367 KEARLPVIENKVCNRYEYLNGRVKSTELCAGDLAGGTDSCQGDSGGPLVCFEKD 420	193 RNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLCLEPD 252	311PSRADIALLKLSSPAVITDEVIPACLPSPNYVVADKTVCYITGWGETQGTFGVGRL 366	138 YNHYSOGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTSD-APGTL 192	255 HFCGGTLISPEWVLTAAHCLDSILGPSFYTVILGAHYEMAREASVQEIPVSRLFLE 310	78 HICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQLPRA 137

Search completed: January 6, 2004, 10:03:10 Job time: 22 secs

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Result
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/ cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep: *
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/ cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep: *
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-10-145-087A-13	US-10-017-086A-132	-10-013-922A-13	-09-999-829A-13	-09-978-681A-13	-09-978-194A-13	-10-165-247A-13	-10-160-502A-13	-10-145-124A-13	-10-165-067A-13	-10-164-728A-13	-10-145-017A-13	-10-013-926A-13	-10-145-089A-13	-10-143-029A-13	-10-143-028A-13	-10-017-191A-13	-10-145-128A-13	-10-143-030A-13	-10-017-083A-13	-10-002-967A-13	0-143-031A-13	-09-978-298A-13	-09-978-188A-13	9-978-375A-13	-09-978-643A-13	-09-978-187B-13	-09-978-757A-13	9-999-830A-13	-978-193A-
equence 13	Sequence 132,	equence 13	e 13	equence 13	equence 13	nce 13	Sequence 132,	equence 13	equence 13	13	e 13	nce 13	nce 13	nce 13	equence 13	nce 13	nce 13	nce 13	equence 13	equence 13	Sequence 132,								
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## ALIGNMENTS

US-09-978-295A-132 Sequence 132, Application US/09978295A Patent No. US20020156006A1 APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585 APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Ashkenazi, Avi APPLICANT: Baker Kevin P. APPLICANT: Botstein, David APPLICANT: APPLICANT APPLICANT INFORMATION: Gurney, Austin L. Hillan, Kenneth J. Kljavin, Ivar J. Kuo, Sophia S. Roy, Margaret Ann Shelton, David L. Stewart, Timothy A. Goddard, Audrey Godowski, Paul J. Grimaldi, J. Christopher Fong, Sherman Gao, Wei-Qiang Gerber, Hanspeter Ferrara, Napoleon Filvaroff, Ellen Tumas, Daniel Pan, James; Gerritsen, Mary E Eaton, Dan Desnoyers, Luc Paoni Napier, Mary A. Nicholas F Nucleic

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LCATION NG DATE LICATION	TILING DATE  FPLICATION FPLICATIO	PPLICATION
NUMBER: 1998-05 NUMBER: 1998-05 NUMBER: 1998-05 NUMBER: 1998-05 NUMBER: 1998-05 NUMBER: 1998-05 NUMBER: 1998-05 NUMBER:	NUMBER: 60/083 1998-04-29 NUMBER: 60/083 1998-04-29 NUMBER: 60/083 NUMBER: 60/083 1998-04-29 NUMBER: 60/083 1998-04-39 NUMBER: 60/083 1998-04-30 NUMBER: 60/083 1998-04-30 NUMBER: 60/084 1998-05-06 NUMBER: 60/084 1998-05-06 NUMBER: 60/084 1998-05-06 NUMBER: 60/084	1998-04-0   1998-04-0   NUMBER: 60   1998-04-1   NUMBER: 60   1998-04-1   NUMBER: 60   1998-04-1   NUMBER: 60   1998-04-2   NUMBER: 60   1998-04-2

PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-03
PRIOR PRIOR PRIOR PRIOR 1997-11-03
PRIOR PRIOR APPLICATION NUMBER: 60/06531
PRIOR APPLICATION NUMBER: 60/06531
PRIOR APPLICATION NUMBER: 60/077450
PRIOR APPLICATION NUMBER: 60/077641
PRIOR APPLICATION NUMBER: 60/077649
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078936
PRIOR APPLICATION NUMBER: 60/078936
PRIOR PRILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079636
PRIOR PRILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079664
PRIOR APPLICATION NUMBER: 60/079786
PRIOR APPLICATION NUMBER: 60/079664
PRIOR APPLICATION NUMBER: 60/079664
PRIOR APPLICATION NUMBER: 60/079664
PRIOR APPLICATION NUMBER: 60/080105
PRIOR APPLICATION NUMBER: 60/08

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RESULT 2
US-09-978-697-132
Sequence 132, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085700
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085689
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085579
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APPLICATION NUMBER: 60/085704
FILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/085573
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APPLICATION NUMBER: 60/085580
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APPLICANT: Hillan, Kenneth J
APPLICANT: KU, Sophia S.
APPLICANT: KU, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Pan, James;
APPLICANT: Pan, James;
APPLICANT: Pan, James;
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Pol
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: 09/9978,697
CURRENT APPLICATION NUMBER: 09/91885
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/064249
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OR FILING DATE: 1998-03-12
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OR APPLICATION NUMBER: 60/078886
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078936
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078910
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DR APPLICATION NUMBER: 60/079294
DR FILING DATE: 1998-03-25
DR APPLICATION NUMBER: 60/079656
DR FILING DATE: 1998-03-26
DR APPLICATION NUMBER: 60/079664
DR FILING DATE: 1998-03-27
DR APPLICATION NUMBER: 60/079689
DR APPLICATION NUMBER: 60/079689
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APPLICATION NUMBER: 60/079663
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APPLICATION NUMBER: 60/079728
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FILING DATE: 1998-03-11
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Grimaldi, J. Christopher
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FILLING DATE: 1998-04-01
APPLICATION NUMBER: 60/080333
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080334

DR FILING DATE: 1998-03-31

DR APPLICATION NUMBER: 60/080107

DR APPLICATION NUMBER: 60/080165

DR FILING DATE: 1998-03-31

DR APPLICATION NUMBER: 60/080194

OR APPLICATION NUMBER: 60/080194

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OR APPLICATION NUMBER: 60/080327

OR FILING DATE: 1998-04-01

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OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/084600
OR FILING DATE: 1998-5-07
OR APPLICATION NUMBER: 60/084627
OR APPLICATION NUMBER: 60/084643
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/08533
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/08533
OR APPLICATION NUMBER: 60/08533
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085323
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OR APPLICATION NUMBER: 60/085323
OR APPLICATION NUMBER: 60/08523
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R APPLICATION UNMBER: 60/08
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/08
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                                                      DSGGPVLCLEPDCHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP
                                                                                                                    WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG
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ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC
                                  DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP
                                                                                                 WDQDTSDAPGTLRNLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG
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Pred. No. 4.4e-245;
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OR APPLICATION NUMBER: 60/081203
OR APPLICATION NUMBER: 60/081203
OR APPLICATION NUMBER: 60/081229
OR FILING DATE: 1998-04-09
OR APPLICATION NUMBER: 60/081955
OR APPLICATION NUMBER: 60/081817
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OR APPLICATION NUMBER: 60/08183
OR APPLICATION NUMBER: 60/08256
OR FILING DATE: 1998-04-21
OR APPLICATION NUMBER: 60/08256
OR FILING DATE: 1998-04-21
OR APPLICATION NUMBER: 60/08270
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630PLC9
CURRENT APPLICATION UNMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/06311
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/070450
PRIOR APPLICATION NUMBER: 60/070450
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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Williams, P. Mic
Wood, William I
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Grimaldi, J. Christopher
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Shelton, David L.
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10, Sophia S.
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DR FILING DATE: 1998-04-08
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DR FILING DATE: 1998-03-27
DR APPLICATION NUMBER: 60/079920
DR FILING DATE: 1998-03-30
DR APPLICATION NUMBER: 60/079923
DR FILING DATE: 1998-03-30
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DR APPLICATION NUMBER: 60/080105
DR APPLICATION NUMBER: 60/080107
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APPLICATION NUMBER: 60/081838
FILING DATE: 1998-04-15
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FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081955
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FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/080194
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APPLICATION NUMBER: 60/079656
FILING DATE: 1998-03-26
APPLICATION NUMBER: 60/079664
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APPLICATION NUMBER: 60/081819
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APPLICATION NUMBER: 60/081817
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PRIOR FILLING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
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                 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC
                                                                                                                                                                               FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC
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SLDWQVYFAEEPEPEAEPGSCLANISQPTSC
                                                                 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS
                                                                                                         LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM
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                                                   VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS
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RESULT 4
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Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi APPLICANT
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APPLICANT APPLICANT: APPLICANT: APPLICANT: APPLICANT:
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APPLICANT: APPLICANT: APPLICANT: APPLICANT: Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A. Fong, Suc.... Gao, Wei-Qiang Ashkenazi, Avi Baker Kevin P. Botstein, David Ferrara, Na Filvaroff, Gerritsen, Mary E. Goddard, Audrey Godowski, Paul J. Grimaldi, J. Christopher Gerber, Eaton, Dan Desnoyers, Luc Hanspeter Napoleon f, Ellen

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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
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OR FILING DATE: 1998-03-31
OR APPLICATION NUMBER: 60/080165
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OR APPLICATION NUMBER: 60/080194
OR FILING DATE: 1998-03-31
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FILING DATE: 1997-11-03
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FILING DATE: 2001-07-30
APPLICATION NUMBER: 60/062250
FILING DATE: 1997-10-17
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FILING DATE: 1998-03-25
APPLICATION NUMBER: 60/079656
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FILING DATE: 1998-03-13
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FILING DATE: 1997-11-21
APPLICATION NUMBER: 60/077450
FILING DATE: 1998-03-10
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079689
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FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080107
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APPLICATION NUMBER: 60/
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Poy, Margaret /
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OR APPLICATION NUMBER: 60/082797
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OR APPLICATION NUMBER: 60/082796
OR FILING DATE: 1998-04-23
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OR APPLICATION NUMBER: 60/082568
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OR APPLICATION NUMBER: 60/082804
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DR FILING DATE: 1998-04-09
DR FILING DATE: 1998-04-15
DR FILING DATE: 1998-04-15
DR APPLICATION NUMBER: 60/081817
DR FILING DATE: 1998-04-15
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PR FILING DATE: 1998-04-30
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PR APPLICATION NUMBER: 60/084366
PR FILING DATE: 1998-05-05
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FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081838
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APPLICATION NUMBER: 60/081195
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081203
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FILING DATE: 1998-05-06
APPLICATION NUMBER: 60/084637
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APPLICATION NUMBER: 60/084639
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APPLICATION NUMBER: 60/083559
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APPLICATION NUMBER: 60/081071
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FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080334
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SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG
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                                                                    VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS
                                                                                                                                    LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM
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                                  VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS
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PRIOR APPLICATION NUMBER: 09/918585
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C7
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CURRENT FILING DATE: 2001-10-15
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J.
Kljavin, Ivar J.
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Shelton, David L.
Stewart, Timothy A.
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Gerritsen, Mary E.
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Filvaroff,
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Desnoyers, Luc
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f, Ellen
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OR APPLICATION NUMBER: 60/084598

OR FILING DATE: 1998-05-07

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OR APPLICATION NUMBER: 60/084627

OR APPLICATION NUMBER: 60/084633

APPLICATION NUMBER: 60/084633

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OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083742
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OR FILING DATE: 1998-04-30
OR FILING DATE: 1998-05-05
R APPLICATION NUMBER: 60/085580
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FILING DATE: 1998-05-06
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FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085579
FILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/083558
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APPLICATION NUMBER: 60/083554
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APPLICATION NUMBER: 60/083545
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083495
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밁 Ş 밁 á Query Match Best Local S Matches 571 61 61 ч Н h 100.0%; Similarity 100.0%; 71; Conservative C MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 0 Score 3108; Pred. No. 4.4 ); Mismatches DB 11; 4.4e-245; es 0; Indels Length 571; 0, Gaps 120 60 60 0

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APPLICANT: Hilan, Kenneth J
APPLICANT: KU, Sophia S.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Pan, James;
APPLICANT: Pan, James;
APPLICANT: Shelton, David L.
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, p. Mickey
APPLICANT: Wunas, Daniel
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Pol
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C22
CURRENT APPLICATION NUMBER: US/09/978,608A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Pal
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US-09-978-608A-132
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napolec
APPLICANT: Filvaror, Eller
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspete
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J
Kuo, Sophia S.
Napier, Mary A.
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US-09-978-608A-132
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; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo s
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Best Local Similarity
Matches 571; Conserv
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                         SLDWQVYFAEEPEPEAEPGSCLANISQPTSC
                                                                                        VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS
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                                                              SGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS
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WESULT 7

US-09-978-585A-132

Sequence 132, Application US/09978585A
Publication No. US20030049633A1

GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Botstein, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Ferrara, Napoleon
APPLICANT: Forng, Sherman
APPLICANT: Goo, Wei-Qiang
APPLICANT: Goo, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gorimaldi, J. Christopher
APPLICANT: Gourney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.

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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/978,585A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper
SEQ ID NO 132
LENGTH: 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C15
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                 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC
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SLDWQVYFAEEPEPEAEPGSCLANISQPTSC
                                                              VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS
                                                                                     VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS
                                                                                                                                LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM
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Shelton, David L.
Stewart, Timothy A.
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RESULT 8
US-09-978-191A-132
; Sequence 132, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:

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APPLICANT Goddard, Audrey
APPLICANT Godowski Paul J.
APPLICANT Grimaldi, J. Christopher
APPLICANT Grimaldi, J. Christopher
APPLICANT Grimaldi, J. Christopher
APPLICANT Hillan, Kenneth J
APPLICANT Hillan, Kenneth J
APPLICANT Kljavin, Ivar J.
APPLICANT Napier, Mary A.
APPLICANT Pan, James;
APPLICANT Pan, James;
APPLICANT Roy, Margaret Ann
APPLICANT Shelton, David L.
APPLICANT Stewart, Timothy A.
APPLICANT Stewart, Timothy A.
APPLICANT Williams, P. Mickey
APPLICANT Williams, P. Mickey
APPLICANT Williams, P. Mickey
APPLICANT Wood, William I.
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C4
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PRIOR TILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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CURRENT FILING DATE: 2001-10-15
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PRIOR TILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/079294
OR FILING DATE: 1998-03-25
OR APPLICATION NUMBER: 60/079656
OR FILING DATE: 1998-03-26
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079669
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079663
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OR APPLICATION NUMBER: 60/079663
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OR APPLICATION NUMBER: 60/079663
OR FILING DATE: 1998-03-27
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OR APPLICATION NUMBER: 60/077632
OR FILING DATE: 1998-03-11
OR APPLICATION NUMBER: 60/077641
OR FILING DATE: 1998-03-11
OR APPLICATION NUMBER: 60/077649
OR APPLICATION NUMBER: 60/077791
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OR FILING DATE: 1998-03-12
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APPLICATION NUMBER: 60/078936
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078910
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FILING DATE: 1997-11-21
APPLICATION NUMBER: 60/077450
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FILING DATE: 1998-03-13
APPLICATION NUMBER: 60/078886
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Baker Kevin P.
Botstein, David
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Gerritsen, Mary E
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Gao, Wei-Qiang
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Filvaroff,
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f, Ellen
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OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079786
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079920
OR FILING DATE: 1998-03-30
OR APPLICATION NUMBER: 60/079923

FILING DATE: 1998-03-30
APPLICATION NUMBER: 60/080105
FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080107

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REFILING DATE: 1998-05-07

OR APPLICATION NUMBER: 60/08

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OR APPLICATION NUMBER: 60/08

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FILING DATE: 1998-05-05
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                                                                                                                                                                         TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL
                                                 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG
                                                                                         SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG
                                                                                                                                                    TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL
DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP
                                WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG
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Pred. No. 4.4e-245;
Mismatches 0;
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OR FILING DATE: 1998-03-31
OR APPLICATION NUMBER: 60/080165
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OR APPLICATION NUMBER: 60/080327
OR FILING DATE: 1998-04-01
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OR FILING DATE: 1998-04-01
OR APPLICATION NUMBER: 60/080333
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OR APPLICATION NUMBER: 60/081070
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OR APPLICATION NUMBER: 60/081071
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OR FILING DATE: 1998-04-09
OR APPLICATION NUMBER: 60/081955
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OR APPLICATION NUMBER: 60/081819
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OR APPLICATION NUMBER: 60/082569
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OR FILING DATE: 1998-04-22
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OR FILING DATE: 1998-04-22
OR APPLICATION NUMBER: 60/083336
OR APPLICATION NUMBER: 60/083322
OR APPLICATION NUMBER: 60/083322
OR APPLICATION NUMBER: 60/08392
OR APPLICATION NUMBER: 60/083495
OR APPLICATION NUMBER: 60/083495
OR APPLICATION NUMBER: 60/083496
OR FILING DATE: 1998-04-29

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RESULT 9
US-09-978-403A-132
Sequence 132, App.
Publication No. U.
APPLICANT: ROY, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C17
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/063311
PRIOR APPLICATION NUMBER: 60/06364
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/06364
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/06364
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Gerritsen, Mary E.
Goddard, Audrey
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Filvaroff, Ellen
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Botstein, David
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Kljavin, Ivar J.
Kuo, Sophia S.
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DR APPLICATION NUMBER: 60/080165

DR FILING DATE: 1998-03-31

DR APPLICATION NUMBER: 60/080194

DR FILING DATE: 1998-03-31

DR APPLICATION NUMBER: 60/080327

DR FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/080105
EILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080107
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APPLICATION NUMBER: 60/079663
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/079656
FILING DATE: 1998-03-26
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APPLICATION NUMBER: 60/078939
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/079294
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APPLICATION NUMBER: 60/
FILING DATE: 1998-04-09
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APPLICATION NUMBER: 60/081195
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APPLICATION NUMBER: 60/081203
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FILING DATE: 1998-04-15
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                                                               APPLICATION NUMBER: 60/081819
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DR FILING DATE: 1998-04-15

BR APPLICATION NUMBER: 60/082568

DR FILING DATE: 1998-04-21

DR APPLICATION NUMBER: 60/082569

DR FILING DATE: 1998-04-21

DR APPLICATION NUMBER: 60/082704

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FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082804
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APPLICATION NUMBER: 60/082700

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RESULT 10
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APPLICANT: Ashkenazi
APPLICANT: Baker, K
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           Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christ
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                                                                 Gao, Wei
Gerber,
                                                                                         Fong,
                                                                                                       Ferrara, Napoleon
Filvaroff, Ellen
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i, Paul J.
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Austin L.
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Pred. No. 4.4e-245;
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Kljavin,
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Shelton, David L.
Stewart, Timothy A.
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Wood, William I
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APPLICATION NUMBER: 60/081819
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APPLICATION NUMBER: 60/080333
                    FILING DATE: 1998-05-05
APPLICATION NUMBER: 60/084414
FILING DATE: 1998-05-06
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FILING DATE: 1998-04-30
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FILING DATE: 1998-04-22
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OR APPLICATION NUMBER: 60/084637
OR APPLICATION NUMBER: 60/084639
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/084640
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OR APPLICATION NUMBER: 60/084627
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OR APPLICATION NUMBER: 60/085339
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085339
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085323
OR APPLICATION NUMBER: 60/085582
OR APPLICATION NUMBER: 60/085582
OR APPLICATION NUMBER: 60/085570
OR FILING DATE: 1998-05-15
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OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085573
OR APPLICATION NUMBER: 60/085704
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LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM
                     LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTTLLGPRACSRLHAAPGGDGSPILPGM
                                                                        FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC
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                                                                                                                                                                                      ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC
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Pred. No. 4.4e-245;
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RESULT 11
US-09-999 833A-132
Sequence 132, App
Sequence 130, No. 1
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembran
TITLE OF INVENTION: Secreted and Transmembran
TITLE OF INVENTION: Acids Encoding the Same
FILL REFERENCE: P2630P1C65
CURRENT APPLICATION NUMBER: U9/09/999,833A
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILLING DATE: 1997-10-17
PRIOR PILLING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/06331
PRIOR APPLICATION NUMBER: 60/06364
PRIOR FILLING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILLING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILLING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR APPLICATION NUMBER: 60/07764
PRIOR FILLING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/07764
PRIOR FILLING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/07764
PRIOR FILLING DATE: 1998-03-12
PRIOR FILLING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/07789
PRIOR FILLING DATE: 1998-03-12
PRIOR FILLING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/077896
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILLING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
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APPLICANT: AShkenazi
APPLICANT: Baker Ke
APPLICANT: Botstein
APPLICANT: Desnoyer
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Hillan, Kenneth
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Godowski, Paul
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Stewart, Timothy A.
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Grimaldi, J. Christopher
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o. US20030054405A1
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Sophia S.
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Kenneth J
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INVENTION: Acids Encoding the Same
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Grimaldi,
                                                                                       Williams, P. Mickey Wood, William I.
                                                                                                                                                                  Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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                                                                                                                                                                                                                                                                                             Pan,
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Botstein, David
                                                                                                                                                Tumas, Daniel
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Hillan, Kenneth J
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J. Christopher
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PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-31
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR APPLICATION NUMBER: 60/077641
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OR APPLICATION NUMBER: 60/078936
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078936
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/079936
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/079294
OR FILING DATE: 1998-03-26
OR APPLICATION NUMBER: 60/079294
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OR APPLICATION NUMBER: 60/07966
OR APPLICATION NUMBER: 60/07972
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OR APPLICATION NUMBER: 60/07992
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/07992
OR APPLICATION NUMBER: 60/080105
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OR APPLICATION NUMBER: 60/08033
OR APPLICATION NUMBER: 60/08033
OR FILING DATE: 1998-04-01
OR APPLICATION NUMBER: 60/08033
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OR APPLICATION NUMBER: 60/082568
OR FILING DATE: 1998-04-21
OR APPLICATION NUMBER: 60/082569
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OR APPLICATION NUMBER: 60/082569
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OR APPLICATION NUMBER: 60/082704
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OR FILING DATE: 1998-04-29

OR APPLICATION NUMBER: 60/083559

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OR APPLICATION NUMBER: 60/083742

OR APPLICATION NUMBER: 60/083742

OR APPLICATION NUMBER: 60/084366

OR FILING DATE: 1998-04-30

OR APPLICATION NUMBER: 60/084414

OR FILING DATE: 1998-05-06

OR APPLICATION NUMBER: 60/084441

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OR APPLICATION NUMBER: 60/084637

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OR FILING DATE: 1998-05-07

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OR APPLICATION NUMBER: 60/083336
OR FILING DATE: 1998-04-27
OR APPLICATION NUMBER: 60/083322
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OR APPLICATION NUMBER: 60/08392
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DR APPLICATION NUMBER: 60/082797

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FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081955
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APPLICATION NUMBER: 60/082804
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OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/08538
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085323
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OR APPLICATION NUMBER: 60/085582
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                                                                                                                                                             LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM
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SLDWQVYFAEEPEPEAEPGSCLANISQPTSC
                         SLDWQVYFAEEPEPEAEPGSCLANISQPTSC
                                                                                        VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS
                                                                                                                                       LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM
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; Publication No. US20030055216A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi RESULT 13

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Shelton, David L.
Stewart, Timothy A.
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Kuo, Sophia S.
Napier, Mary A.
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Hillan, Kenneth J
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Grimaldi, J. Christopher
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Gerritsen, Mary E.
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ff, Ellen
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FILING DATE: 1998-04-15
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FILING DATE: 1998-04-15
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OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/084640
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084643
FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/083742
FILING DATE: 1998-04-30
APPLICATION NUMBER: 60/084366
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APPLICATION NUMBER: 60
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FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/084441
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                                                     WDQDTSDAPGTLRNLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG
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CURRENT APPLICATION UNMBER: US/09/918,585A
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-03
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APPLICATION NUMBER: 60/077450 FILING DATE: 1998-03-10 APPLICATION NUMBER: 60/077632 FILING DATE: 1998-03-11 APPLICATION NUMBER: 60/077641
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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                                                                                                                                                                                                                                                                                                                 Williams, P. Mickey Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                                                   Tumas, Daniel
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Filvaroff, Ellen
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Desnoyers, Luc
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                                                                                                                                                                                                                                                                                                                                                                                                                           Paoni,
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                                                                                                                                                                                                                                                                                                                                                                                                                                             James;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Nicholas F
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mary A.
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OR FILING DATE: 1998-03-12
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OR FILING DATE: 1998-03-12
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OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078936
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078936
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/07966
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/07966
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OR APPLICATION NUMBER: 60/07966
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/07978
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OR APPLICATION NUMBER: 60/08033
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OR APPLICATION NUMBER: 60/08107
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OR APPLICATION NUMBER: 60/08107
OR APPLICATION NUMBER: 60/08107
OR APPLICATION NUMBER: 60/08120
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GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Beststein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Besnoyers, Luc
APPLICANT: Ferrara, Napole
APPLICANT: Filvaroff, Elle
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Mary
APPLICANT: Godowski, Paul
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, J. Ch
APPLICANT: Grimaldi, J. Ch
APPLICANT: Gurney, Austin
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US-09-978-423A-132
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Matches 571
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DR APPLICATION NUMBER: 60/085704
DR FILING DATE: 1998-05-15
DR APPLICATION NUMBER: 60/085697
DR FILING DATE: 1998-05-15
DR APPLICATION NUMBER: 60/086023
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     Gerritsen, Mary E.
Goddard, Audrey
Goddwski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Gao, Wei-Qiang
Gerber, Hanspeter
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Botstein, David
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llarity 100.0%; !
Conservative 0;
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                                                                                                                                                                                                                                                  ff, Ellen
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Pred. No. 4.4e-245;
); Mismatches 0;
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OR APPLICATION NUMBER: 60/07791
OR APPLICATION NUMBER: 60/078806
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OR APPLICATION NUMBER: 60/078936
OR APPLICATION NUMBER: 60/078936
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078936
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078939
OR APPLICATION NUMBER: 60/078939
OR APPLICATION NUMBER: 60/079294
OR FILING DATE: 1998-03-25
OR APPLICATION NUMBER: 60/079294
OR APPLICATION NUMBER: 60/079656
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OR FILING DATE: 1998-03-27
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OR APPLICATION NUMBER: 60/079920
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DR FILING DATE: 1997-11-13
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OR FILING DATE: 1997-10-17
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PR FILING DATE: 1998-04-01

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VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS
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US-09-387-375-9
US-09-386-655A-9
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US-09-386-629-7
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US-08-481-938-1
US-08-665-785-1
US-08-66-785-1
US-08-66-785-1
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US-08-866-735-1
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Sequence 7, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 66, Appl
Sequence 12, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 10, Appli
Sequence 13, Appli
Sequence 1, Appli
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227 CGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWL CAGFEEGKKDACKGDSGGPLVCLVGQS-WLQAGVISWGEGCARQNRPGVYIRVTAHHNWI

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214

GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon,
APPLICANT: Qi, Jenson

Patricia

RESULT 2 US-09-387-375-7

Sequence 7, Application US/09387375 Patent No. 6485957

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	MYARVI MI MGSPSI	EEVGV/	OMAMS 	ilarity Conserva	sapiens	DATE: D NOS:	row, Andre Jian-shen ION: DNA e ION: prot	ი 	C)		1.4.	4, 4	ۍ i	יט פט	თ თ		თ თ		י סי פ	ש פע	<b>თ</b> თ	
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	PGPHAMYARVRQVESNPLYQGTASSADVALVELEAPVPFTNYILPVCLPDPSVI CWATGWDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNP	PGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT-	NTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREG            ::   :                   :     :  :  :	Score Pred. 44; Mis		US/09/386 )8-31	ling the	ricia	36653A	ALIG	US-09-7	US-08-9	US-08-9	5200340 US-09-5			US-08-991-7 US-07-854-6	, ,		1 )	US-09-6	
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	RPGMLDML	PFGAS	WSVVLGSLQREG :  :  :   YQVLLGARQLVQ	Gaps						•	4, Appl		778		i, App	29, Ap	6, Appli 2, Appli	l, App	App	54, Ap	i, App hpp	
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-387-375-7
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CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/387,375
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 316
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Patent No. 6485957
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: DNA Encoding the Human Serine TITLE OF INVENTION: Protease EOS FILE REFERENCE: ORT-1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Darrow, Andrew APPLICANT: Andrade-Gordon, APPLICANT: Qi, Jenson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: DNA Encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE:
                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: sequence of EOS zymogen fusion gene
                                                                                                                                                                          Local Similarity
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                                  124 AEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWAT
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                                                                                                 64 GEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPG
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                                                                             GEWPWQASIQHPGAHVCGGSLIAPQWVLTAAHCFPRRALPA--EYRVRLGALRLGSTSPR 118
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TLSVPVRRVLLPPDYSEDGARGDLALLQLRRPVPLSARVQPVCLPVPGARPPPGTPCRVT
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40.7%; Pred. No. 4.1e-31;
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40.7%; Pred. No. 3.5e-31;
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US-08-944-483-66

Sequence 66, Patent No. 6

Application US/08944483

GENERAL INFORMAPPLICANT:
APPLICANT:
APPLICANT:

INFORMATION:

COHEN,

MAURICE

APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:

INVENTION:

NOVEL SERINE

COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GRANADOS, EDWARD N.
KLASS, MICHAEL R.
RUSSELL, JOHN C.
STEWART, KENT D.
STROUPE, STEVEN D.

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SEQ ID NO 9
LENGTH: 315
TYPE: PRT
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/386,653A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: ORT-1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: DNA encoding the novel human serine TITLE OF INVENTION: protease T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Andrade-Gordon, APPLICANT: Darrow, Andrew APPLICANT: Qi, Jian-shen
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                EEGKKDACKGDSGGPLVCLVGQS-WLQAGVISWGEGCARQNRPGVYIRVTAHHNWI
                                                                               QPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWL 286
                                                                                                                GWGSPSEEDLLPEPRILQKLAVPIIDTPKCNLLYSKDTEFGYQPKTIKN----DMLCAGF
                                                                                                                                               GW----DQDTSDAPGTLRNLRLISRPTCNCIYNQ-----LHQRHLSNPARPGMLCGGP
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                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     Description of Artificial Sequence: Fusion Protein of Protease T in a zymogen activation construct
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Pred. No. 5e-31;
3; Mismatches
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STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: N
US-08-944-483-66
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US-09-386-642-12
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Sequence 12, Application US/09386642 Patent No. 6420157 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 61
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Becker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Abbott Park
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                                                                                                                                                                                                                                                                                                                                       172 FGASCWATGWDQDTSD----APGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLC 227
                                                                                                                                                                                                                                                                                                                                                                                                   120 LSPGAEEVGVAALQ--LPRAYNHYSQGS--DLALLQLAHPTTHT----PLCLPQPAHRFP
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                                                                                                                                                                                                                                                                                                                                                                     64 YS---EDAKVSTLKDIIPHP-SYLQEGSQGDIALLQLSRPITFSRYIRPICLPAANASFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 NTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                   6 SAVAGQWPWQVSITYEGVHVCGGSLVSEQWVLSAAHCFPSEHHKE--AYEVKLGAHQLDS
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                                                                                                                                                                                                           ARV---QGAAFLAQSPETPEMSDEDSCVACGS----
                                                                                                                                                                                                                                                                      GGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 287
                                                                                                                                               SPW 330
                                                                                                                                                                           SKVTELQPRVV----PQTQE-SQPDSNL-CGSHLAFSSAPAQGLLRPILFLPLGLALGLL 292
                                                                                                                                                                                                                                                                                                         NGLHCTVTGWGHVAPSVSLLTPKPLQQLEVPLISRETCNCLYNIDAKPEEPHFVQEDMVC 179
                                                                                                                                                                                                                                          AGYVEGGKDACQGDSGGPLSC-PVEGLWYLTGIVSWGDACGARNRPGVYTLASSYASWIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.8%; Score 429.5; DB 3 35.6%; Pred. No. 1.3e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES OF THE PROSTATE
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APPLICANT: Qi, Jenson
APPLICANT: Qi, Jenson
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Q1, Jenson
APPLICANT: Q1, Jenson
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILLNG DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                          SEQ ID NO 11
LENGTH: 328
                                                                               Matches
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Patent No. 6420157
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Best Local Similarity
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                                                                                                    Best
                                                                                                                  Query Match
                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Fusion OTHER INFORMATION: with homo sapien serine protease catalytic
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 AEEVGVAALQ--LPRAYNHYSQGS--DLALLQLAHPTTHT----PLCLPQPAHRFPFGAS 175
                                                                               100;
61
                               64 GEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 GOWPWQVSITYEGVHVCGGSLVSEQWVLSAAHCFPSEHHKE--AYEVKLGAHQLDSYS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 GEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPG
                                                                                               Similarity
GOWPWOVSITYEGVHVCGGSLVSEOWVLSAAHCFPSEHHKE--AYEVKLGAHQLDSYS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- QGAAFLAQSPETPEMSDEDSCVACGS 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CWATGWDQDTSD----APGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGGKDACQGDSGGPLSC-PVEGLWYLTGIVSWGDACGARNRPGVYTLASSYASWIQSKVT
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                                                                               Conservative
                                                                                             13.6%;
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                                                                                               Score 422; DB 4;
Pred. No. 6.6e-29;
                                                                               Mismatches
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; Sequence 8, Application US/09386629 ; Patent No. 6426199
                                                          RESULT 9
US-09-386-629-8
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US-09-386-629-7
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APPLICANT: Qi, Jenson
APPLICANT: Qi, Jenson
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: NUENTION: Idenification and Characterization of the complementary
TITLE OF INVENTION: DNA encoding the novel human serine protease C-E
FILE REFERENCE: ORT-1030
CURRENT APPLICATION NUMBER: US/09/386,629
CURRENT FILING DATE: 199-08-31
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
LENGTH: 317
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Match 12.9%; Score 400; DB 4; Length 317; Local Similarity 30.8%; Pred. No. 5.3e-27; les 99; Conservative 57; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                      186
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                                                                                                                                                                                  SDEDSCVACGSLRTAGPQAGA 326
                                                                                                                                                                                                                         LMC-QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQ-----
                                                                                                                                                                                                                                                                    VLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPETPEM
                                                                                                                                                                                                                                                                                                           LPHPQTLQKLKVPIIDSEVCSHLY---WRGAGQGPITEDMLCAGYLEGERDACLGDSGGP
                                                                                                                                                                                                                                                                                                                                                  SDAPGTLRNLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGP 245
                                                                                                                                                                                                                                                                                                                                                                                                                                      RAYNHYSQG--SDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGW----DQDT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQKNGTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CWATGWDQDTSD----APGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -EDAKVSTLKDIIPHP-SYLQEGSQGDIALLQLSRPITFSRYIRPICLPAANASFPNGLH
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                                                                                                                                            -----GGGALRAPSQGSGA 313
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Sequence 10, Application US/09644600
Patent No. 6451500
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Pro
TITLE OF INVENTION: Overexpressed in Carcinomas
FILE REFERENCE: D6064CIP/D
CURRENT APPLICATION NUMBER: US/09/644,600
CURRENT FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/421,213
PRIOR APPLICATION NUMBER: 09/421,213
PRIOR APPLICATION NUMBER: 09/027,337
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: 09/027,337
PRIOR FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 98
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                                                                                     ; OTHER INFORMATION: US-09-644-600-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 8
LENGTH: 327
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
Query Match
Best Local Similarity
Matches 92; Conserva
                                                                                                                                                                                                                       SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
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APPLICANT: Q1, Jenson
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Idenification and Characterization of the complementary
TITLE OF INVENTION: DNA encoding the novel human serine protease C-E
FILE REFERENCE: ORT-1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/386,629
CURRENT FILLING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                        LENGTH: 902
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                               FEATURE:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 PGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 CWATGW----DQDTSDAPGTLRNLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 SRSQKVGVAWVE-PHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 PGAEEVGVAALQLPRAYNHYSQG--SDLALLQLAHPTTHT----PLCLPQPAHRFPFGAS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 EWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNS---WSVVLGSLQREGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 EWPWIVSIQKNGTHHCAGSLLTSRWVITAAHCFK----DNLNKPYLFSVLLGAWQLGNPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CWISGWGSIQDGVPLPHPQTLQKLKVPIIDSEVCSHLY---WRGAGQGPITEDMLCAGYL
  Conservative
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                                                                                                        Epithin
                  12.1%; Score 375; DB 4; Length 902; 33.3%; Pred. No. 3.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.5%; Score 388; DB 4; 32.7%; Pred. No. 6.2e-26; tive 49; Mismatches 102
38;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102;
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  Indels
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32;
Gaps
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                                                                                                                   Query Match
Best Local S
Matches 90
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APPLICANT: Soff,
                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 1642
ATTORNEY/AGENT INFORMATION:
NAME: Crook, Wannell M.
REGISTRATION NUMBER: 31,071
REFERENCE/DOCKET NUMBER: 3501
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gately, Stephen APPLICANT: Twardowski, Prze
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: "Methods and Compositions for Generating TITLE OF INVENTION: Angiostatin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIÚM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                   Local Similarity
nes 90; Conser
                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sheridan Ross P.C. STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                        LENGTH: 790 amino acids
                                          531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 YNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              608 SFTK----QARVVGGTNADEGEWPWQVSLHALGQGHLCGASLISPDWLVSAAHCFQDDKN 663
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74 RQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQ 133
                                                                            23 LYDFCIV--CITTYAINVSLMWLSF----RKVQEPQGKAKRHGN--TVPGEWPWQASVR- 73
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                                      LFDYCDVPQCVTS-----SFDCGKPKVEPKKCPARVVGGCVSIPHSWPWQISLRY 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QRNKPGVYTRLPCSSGLDQRAHWGIAAWTDSRPQTP 867
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                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                       863-9700
                                                                                                               11.9%; Score 370.5; DB 4; 32.3%; Pred. No. 7.1e-24; tive 49; Mismatches 101;
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GENERAL INFORMATION:
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                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                         TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 812
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Folkman, Judan
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Angiostatin and Method
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: LATTY W. Stults, Ph.D.
REGISTRATION NUMBER: 34,025
REFERENCE/DOCKET NUMBER: 05213-0120
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: MacInto OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Atlanta
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 661
                                     134
                                                                           603 FTGQHFCGGTLIAPEWVLTAAHCLEKSSRPEF--YKVILGAHEEYIRGLDVQEISVAKLI 660
                                                                                                                                                  551 LYDYCDIPLCASA------SSFECGKPQVEPKKCPGRVVGGCVANPHSWPWQISLRTR 602
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                                                                                                                                                                                                                               93;
                                                                                                                                                                                                                                              Similarity
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                                   LPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGW--DQDTSD 187
                                                                                                      --GAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQ 133
                                                                                                                                                                                       LYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKR-HGNTV-----PGEWPWQASVRRQ 75
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LE-----PNNRDIALLKLSRPATITDKVIPACLPSPNYMVADRTICYITGWGETQGTFG 714
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                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                          404-818-3700
                                                                                                                                                                                                                           11.9%; Score 369.5; DB 32.7%; Pred. No. 9e-24; tive 45; Mismatches 1
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                                                                                                                                                                                                                                                                DB 1;
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US-08-451-932-1
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US-08-451-932-1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 05/26/95
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08
FILING DATE: 04/26/94
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: LAXYY W. Stults, Ph.D.
REGISTRATION NUMBER: 34,025
REFERENCE/DOCKET NUMBER: 05213-0123
RELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: MacIntosh
OPERATING SYSTEM: 7.0
SOFTWARE: Microsoft Word
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ZIP: 30303-1769
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                                   188 APGTLRNLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVL 247
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11.9%; Score 369.5; DB 1; Length 812;
Similarity 32.7%; Pred. No. 9e-24;
93; Conservative 45; Mismatchen 107
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A-GRIKEAQIPVIENKVCNRV-----EYINNRVKSTEICAGQIAGGVDSCQGDSGGPIV 767
                                                                                                                   LPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGW--DQDTSD 187
                                                                                                                                                                                             --GAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQ 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APGTLRNLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVL 247
                                                                            LE-----PNNRDIALLKLSRPATITDKVIPACLPSPNYMVADRTICYITGWGETQGTFG
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191 Peachtree Sti
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/248,629
FILING DATE: 04/26/94
ATTORNEY/AGENT INFORMATION:
NAME: Larry W Stults, Ph.D.
REGISTRATION NUMBER: 34,025
REFERENCE/DOCKET NUMBER: 05213-0124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
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                                                                                                                                                                                                                                                                                                                              23 LYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKR-HGNTV-----PGEWPWQASVRRQ
                                                                                                                                                                                                                                                                                                                                                                   93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30303-1769
                                                                                                                                                                                                                     FTGQHFCGGTLIAPEWVLTAAHCLEKSSRPEF--YKVILGAHEEYIRGLDVQEISVAKLI
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CFEKDKYILQ-GVTSWGLGCARPNKPGVYVRVSRFVDWIEREMR 810
                                CLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQ 291
                                                                        A-GRIKEAQIPVIENKVČNRV-----EYINNRVKSTEICAGQLAGGVDSCQGDSGGPLV 767
                                                                                                         APGTLRNLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVL 247
                                                                                                                                               LE-----PNNRDIALLKLSRPATITDKVIPACLPSPNYMVADRTICYITGWGETQGTFG
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O'Reilly, Michael
WENTION: Method of Diagnosing an Angiogenic
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                                                                                                                                                                                                                                                                                                                                                                 11.9%; Score 369.5; DB 1; 32.7%; Pred. No. 9e-24; ative 45; Mismatches 107;
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RESULT 15
US-08-326-785-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 93; Conserv
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INFORMATION FOR SEQ ID NO:
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LENGTH: 812
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ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50
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APPLICATION NUMBER: US/08/326,785
FILING DATE:
CLASSIFICATION: 424
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APPLICATION NUMBER: 08/248,629
FILING DATE: 04/26/94
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Larry W. Stults, Ph.D.
REGISTRATION NUMBER: 34,025
REFERENCE/DOCKET NUMBER: 05213-0121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: MacIntosh
OPERATING SYSTEM: 7.0
SOFTWARE: Microsoft Word
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ZIP: 30303-1769
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STATE: Georgia
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                                                                                                                                                                                                                                                                                715 A-GRIKEAQIPVIENKVCNRV-----EYINNRVKSTEICAGQLAGGVDSCQGDSGGPLV 767
                                                                                                                                                                                      661 LE-----PNNRDIALLKLSRPATITDKVIPACLPSPNYMVADRTICYITGWGETQGTFG 714
                                                                                                                                                                                                                                                                                                                                                                             551 LYDYCDIPLCASA-----SSFECGKPQVEPKKCPGRVVGGCVANPHSWPWQISLRTR 602
768 CFEKDKYILO-GVTSWGLGCARPNKPGVYVRVSRFVDWIEREMR 810
                                                                                                                                     188 APGTLRNLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVL 247
                                                                                                                                                                                                                                   134 LPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGW--DQDTSD 187
                                                                                                                                                                                                                                                                                                                                                                                                                            23 LYDFCIVCITYAINVSLMWLSFRKVQEPQGKAKR-HGNTV-----PGEWFWQASVRRQ 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                        CLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQ 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.9%; Score 369.5; DB 1; Length 812; 32.7%; Pred. No. 9e-24; tive 45; Mismatches 107; Indels 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 39;
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Search completed: January 6, 2004, 10:03:44
Job time : 22 secs

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

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5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

ø	80	7	o	v	4.	ω	2	11	Result
1454	2304	2779.5	2809.5	2809.5	3108	3108	3108	3108	Score
46.8	74.1	89.4	90.4	90.4	100.0	100.0	100.0	100.0	Query Match Length DB
267	552	642	628	628	571	571	571	571	ength 1
21	23	24	24	23	24	21	21	20	8
AAY90291	AAE21440	ABP72374	ABP72375	AAU82728	ABU61090	AAB24046	AAB44260	AAY41704	ID
Human peptidase, H	Human m32404 prote	Transmembrane seri	Transmembrane seri	Amino acid sequenc	Human PRO351 polyp	Human PRO351 prote	Human PRO351 (UNQ3	Human PRO351 prote	Description

444							10 12 13 14
4444	4448 448 447.5	4444	444	444 449 9	76 49	536.5 636.5 724	1436 1346 1023 1003.5 896.5 885
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222	20033	2221	22 24 24	22 22 22	22343	322222	222222222222222222222222222222222222222
AAU00468 AAB73946 ABB07284	1000	ABG73394 ABU59761 AAW77304	AAB73945 ABG64545 ABU66680 ABU66956	ABB07286 AAY73388 AAU12282 AAE03821	ABB09523 ABB09523 ABU12065 ABP60993 AAM41174	275 275 273 273 273	AAB20156 ABP72373 AAB20162 AAY72095 AAG67515 AAG67514 ABB8135
Recombinant human Fusion protein of Human prostasin-li	human prote human prote e plasminoge	serine pro secreted a acid seque	proteas albumir PRO pol	Ω	Human prostatin pr Human prostatin pr Human NOV12a CG922 Novel human protei Human polypeptide	acid sequent polypeptide protease pp protease pp acid sequent acid sequent protease pp acid sequent protease prote	Human protein SECP Transmembrane seri Human protein SECP Human serine prote Human serine prote Amino acid sequenc Amino acid sequenc

## ALIGNMENTS

RESULT 1 AAY41704

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٠.	••	20-MAR-1998; 98US-0078886.	17-MAR-1998; 98US-0040220.	13-MAR-1998; 98US-0078004.	12-MAR-1998; 98US-0077791.	11-MAR-1998; 98US-0077649.	11-MAR-1998; 98US-0077641.	•	10-MAR-1998; 98US-0077450.		08-MAR-1999; 99WO-US05028.		16-SEP-1999.		WO9946281-A2.		Homo sapiens.		secreted protein; transmembrane protein.	probe; blood coagulation disorder; cancer; cellular adhesion disorder;	Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;	,	Human PRO351 protein sequence.		07-DEC-1999 (first entry)		AAY41704;		AAY41704 standard; Protein; 571 AA.	

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3-0079664 3-0079689 3-0079728

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Best Local &
Matches 571
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28-MAY-1998;
28-MAY-1998;
30-JUL-1998;
11-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes secreted and transmembrane polypeptides and their polynuclectides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AZ33891 to AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
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useful for treating
adhesion disorders .
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DB; AAZ34002.
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                                                       LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM
                                                                                       FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC
                                                                                                    FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC
                                                                                                                                  ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC
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              VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS
                                                                                                                                                                                                                                                                       SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG
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VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS
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98US-0087106.
98US-0087208.
98US-0094651.
98US-0100038.
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Pred. No. 2.5e-207;
Mismatches 0;
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                                  their polynucleotides, cancers and cellular
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27. MAR 1998
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98US-008105-079786.
98US-0080105-98US-0080105-98US-0080165-98US-0080194-98US-0080127-98US-00811070-98US-00811071-98US-00811171-98US-0081117-98US-008111-98US-008111-98US-00811-98US-00811-98US-00811-98US-00811-98US-00811-98US-00811-98US-00811-98US-0081-98US-0081-98US-0081-998US-0

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RESULT 2
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02-DEC-1999;
02-DEC-1999;
16-DEC-1999;
30-DEC-1999;
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30-DEC-1999;
05-JAN-2000;
         AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expressed
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N-PSDB; AAC78486.
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29-OCT-1999;
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23-JUN-1999
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                                                                                                                                                                           vel PRO polypeptides and polynucleotides used in detection methods,
target bioactive molecules to specific cells, and to modulate
llular activities -
isolation of the PRO polynucleotide sequences.
                                                                                                                                                  12; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                secreted protein; transmembrane protein; PRO; EST; cytostatic;
sed sequence tag; detection; cancer.
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                                                                                                                                                                                                                                                                                                                                             GENENTECH INC.
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                                                                                                                                                                                                                                                               AJ, Baker KP,
Filvaroff E,
Godowski PJ,
Kuo SS, Nap,
Stewart TA,
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2000WO-US00219.
2000WO-US00277.
2000WO-US00376.
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99WO-US31243.
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S-0162506.
D-US28313.
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                                                                                                                                                                                                                                                               KP, Botstein D, Desnoyers L, Eaton DL;
E, Fong S, Gao W, Gerber H, Gerritsen ME;
PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
Napier MA, Pan J, Paoni NF, Roy MA;
TA, Tumas D, Williams PM, Wood WI;
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 08-MAR-1999;
12-MAR-1999;
                                    06-JAN-2000;
                                                                                   WO200053754-A1
                                                                                                                                             tumourigenesis; detection; ne cytostatic; antiinflammatory;
                                                                                                                                                                                               Human PRO351
                                                                                                                                                                                                                       25-JAN-2001
                                                                                                                                                                                                                                              AAB24046;
                                                                                                                                                                                                                                                                     AAB24046
                                                                                                                                 immunological disorder.
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                                                                                                                                             tumour; diagnosis; neoplastic disease; identification; can igenesis; detection; neoplastic cell growth; proliferation; atic; antiinflammatory; immunomodulatory; inflammatory diso
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71; Conservative
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                                                                                                                                                                                                                                                                     standard; Protein;
                                                                                                                                                                                                                                                                                                                                SLDWQVYFAEEPEPEAEPGSCLANISQPTSC
                                                                                                                                                                                                                                                                                                                                                       SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
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99US-0123957
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Pred. No. 2.5
0; Mismatches
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                                                                                                                                                                                               NO:12
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Query Match
Best Local Sim:
Matches 571;
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AAC58123 to AAC58224 represent human PRO sequences. AAC58241 and AAB24041 to AAB24056 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
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21-APR-1999
28-APR-1999
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30-NOV-1999
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FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC
                                                                         ETPEMSDEDSCVACGSLRTAGPOAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC
                                                                                                                       ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC
                                                                                                                                                                       DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP
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99WO-US28313.
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99US-0130232.
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Pred. No. 2.5e-207;
0; Mismatches 0;
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30-DEC-1999
05-JAN-2000;
06-JAN-2000;
11-FEB-2000;
11-FEB-2000;
12-FEB-2000;
24-FEB-2000;
10-MAR-2000;
11-MAR-2000;
21-MAR-2000;
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23-JUN-2000;
24-AUG-2000;
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2000WO-US00277
2000WO-US00376
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2000WO-US05004
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2000WO-US06319
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99WO-US05028.
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11-MAR-1998;
11-MAR-1998;
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11-MAR-1998;
12-MAR-1998;
20-MAR-1998;
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N-PSDB;
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25-MAY-2001;
                          Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating cancer, kidney diseases, bone, cartilage disorders and immune deficiencies -
Claim 12; Fig 49; 459pp; English
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)B; ABX92374.
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Filvaroff E,
Godowski PJ,
, Kuo SS, Napi
, Stewart TA,
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98US-079920P.
98US-079923P.
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81US-0267213.
98US-0040220.
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98US-077631P.
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E, Fong S, Gao W, Gerber H, Gerritsen
PJ, Grimaldi JC, Gurney AL, Hillan KJ;
Napier MA, Pan J, Paoni NF, Roy MA;
TA, Tumas D, Williams PM, Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN
                                                                            SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
                                                                                                                              VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS
                                                                                                                                                                                        LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM
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                                                                                                                                                                                                                                                                                                                                                                                                                WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG
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                                                         SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
                                                                                                                                                                    LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM
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                                                                                                                                                                                                                                                                                   ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC
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                                                                                                                                                                                                                                                                                                                                                                                                   WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG
                                                                                                               VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS
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Score 3108; DB 24; Pred. No. 2.5e-207; Mismatches 0;

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Gaps

120 60 60

480

540 480 420

360 360 300

420

300

240 240 180 180 120

571; 0;

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CC The present invention relates to the isolation of novel human CC proteases, and the nucleic acids encoding them. The sequences of CC the invention are useful for treating diseases and disorders such as CC cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. restenosis and coronary thrombosis), brain or neuronal-associated CC diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory CC disorders (e.g. rheumatoid arthritis and psoriasis), central or CC peripheral nervous system diseases, migraines, pain, sexual dysfunction, CC mood disorders, attention disorders, pain, sexual dysfunction, CC mypertension, psychotic disorders, cognition disorders hypotension, CC hypertension, psychotic disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's disease) and dyskinesias.

CC The nucleic acids and polypeptides are also useful for treating viral CC infections such as ocular disease (e.g. glaucoma) and macular accounts of the company of the comp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Charydczak G;
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DB; ABK31770.
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The present sequence is the protein sequence of novel human type II transmembrane serine protease 20 (MTSP20), an endothelial cell transmembrane protein (endotheliase) that is expressed in oesophageal tumour tissues, in lung carcinoma, colon, cervix, leukaemia and other cell lines as well as in certain healthy cells and tissues. The level of MTSP20 can be diagnostic of prostate, uterine, lung, cesophagus or colon cancer, or leukaemia. The expression and/or activation of MTSP20 on, or in the vicinity of, a cell or a bodily fluid can be a marker for breast, prostate, lung, colon and
                                                                                                                                                                                               New type-II membrane-type serine protease 20 polypeptides, useful for preparing a medicament for diagnosing, treating or preventing cancer, dermatological disorders, aberrant wound repairs or crest syndromes -
                                                                                                                                                                                                                                                                  WPI;
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cirrhosis, osteoradionecrosis, postoperative adhesions, pyogenic
granuloma and systemic sclerosis, aberrant wound repairs,
circulatory disorders (especially Raynaud's phenomenon), crest
syndromes (especially calcinosis, oesophageal, dyomotiloty,
sclerodactyly and telangiectasis), dermatological disorders
(especially systemic vasculitis, scleroderma, pyoderma
creation of the post-wine stains, blue rubber bleb naevus
sturge-Weber syndrome, Post-wine stains, blue rubber bleb naevus
syndrome, Klippel-Trenaunay-Weber syndrome and Osler-Weber-Rendu
syndrome) and ocular disorders (especially blindness caused by
coular neovascular disease, corneal graft neovascularisation,
macular degeneration in the eye, neovascular glaucoma, trachoma,
diabetic retinopathy, myopic degeneration, retinopathy of
prematurity, retrolental ribroplasia and corneal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chain forms, the nucleic acids encoding them, probes and primers, expression vectors, host cells, antibodies and transgenic animals. Nucleic acids encoding MTSP20 or its protease domain can be expressed in a host cell, and the protein used in assays to identify candidate compounds that modulate MTSP activity. A claimed method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fractures, periodontitis, psoriasis, rheumatoid arthritis, venous stasis ulcers, granulations burns, hypertrophic scars, liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              angiofibroma, angiolipoma, atherosclerosis, restenosis/reperfusion injury, arteriovenous malformations, haemangiomatosis and vascular adhesion, dyschondroplasia with vascular hamartoma (Fafucci's syndrome), hereditary haemorrhagic telangiectasia (Rendu-Osler-Weber syndrome) and von Hipple Lindau syndrome), chronic inflammatory diseases (especially diabetes mellitus, haemophiliac joints, inflammatory bowel disease, nonhealing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            undesired and/or uncontrolled angiogenesis or neovascularisation, especially undesired angiogenesis associated with solid neoplasms, vascular malformations and cardiovascular disorders (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other cancers. The invention provides MTSP20 polypeptides protease domains, zymogen and activated forms, single and m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HRFPFGASCWATGWDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QRGPGPPKPQEGNTVPGEWFWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNS 164
QPVTLGASLRPLCLPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHA 467
                                                                                                                               LVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLA
                                                                                                                                                                                                                                                                                 ARVQGAAFLAQSPETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HRFPFGASCWATGWDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WSVVLGSLQREGLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPA
                                                                                                                                                                                                                    ARVQGAAFLAQSPETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGA
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Claim 5; Page 212-213; 216pp; English

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; transmembrane serine protease 20; MTSP20; enzyme; endotheliase; cytostatic; dermatological; cardiant; vuln ophthalmological; gene therapy.
                              New type-II membrane-type serine protease 20 polypeptides, useful for preparing a medicament for diagnosing, treating or preventing cancer, dermatological disorders, aberrant wound repairs or crest syndromes -
                                                                         N-PSDB;
                                                                                                                                                    03-JUL-2001; 2001US-302939P
                                                                                                                                                                        03-JUL-2002; 2002WO-US21208
                                                                                                                                                                                               16-JAN-2003.
                                                                                                                                                                                                                   WO2003004681-A2
                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                               Domain
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                                                                                                                                                                                                                                                                                                                                                                                                        Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane serine protease 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP72374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP72374 standard; Protein;
                                                                                                          Madison
                                                                                                                              (CORV-)
                                                                         2003-239207/23.
DB; ABZ58499.
                                                                                                         EL,
                                                                                                                              CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APGGDGSPILPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPA
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                                                                                                                                                                                                                                                                                                                                               specifically 375..376
                                                                                                                                                                                                                                                   /note= "potential N-glycosylation site"
621
                                                                                                                                                                                                                                                                          /note=
77
                                                                                                                                                                                                                                                                                              624..642
                                                                                                                                                                                                                                                                                                      /note= "trypsin-like serine protease domain, specifically described in Claim 9"
                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Signal_peptide
                                                                                                                                                                                                                                        note= "potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                               . 624
                                                                                                                                                                                                                                                                                                                                                                                    . 343
                                                                                                                                                                                                                                                                                                                                                                                             "protease activation cleavage site"
                                                                                                                                                                                                                                                                                   "region specifically described in Claim
                                                                                                                                                                                                                                                                                                                                        "protease activation cleavage site"
                                                                                                                                                                                                                                                                                                                                                             "trypsin-like serine protease domain, specifically described in Claim 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MTSP20).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              628
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angiofibroma, angiolipoma, atherosclerosis, restenosis/reperfusion
cinjury, arteriovenous malformations, haemangiomatosis and vascular
adhesion, dyschondroplasia with vascular hamartoma (Fafucci's
syndrome), hereditary haemorrhagic telangiectasia
(Rendu-Osler-Weber syndrome) and von Hipple Lindau syndrome),
chronic inflammatory diseases (especially diabetes mellitus,
haemophiliac joints, inflammatory bowel disease, nonhealing
fractures, periodontitis, psoriasis, rheumatoid arthritis, venous
stasis ulcers, granulations-burns, hypertrophic scars, liver
cirrhosis, osteoradionecrosis, postoperative adhesions, pyogenic
granuloma and systemic sclerosis), aberrant wound repairs,
circulatory disorders (especially Raynaud's phenomenon), crest
syndromes (especially calcinosis, oesophageal, dyomotiloty,
sclerodactyly and telangiectasis), dermatological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the protein sequence of novel human type

II transmembrane serine protease 20 (MTSP20), an endothelial cell

transmembrane protein (endotheliase) that is expressed in oesophageal

tumour tissues, in lung carcinoma, colon, cervix, leukaemia and other

cell lines as well as in certain healthy cells and tissues. The

level of MTSP20 can be diagnostic of prostate, uterine, lung,

cesophagus or colon cancer, or leukaemia. The expression and/or

activation of MTSP20 on, or in the vicinity of, a cell or a

bodily fluid can be a marker for breast, prostate, lung, colon and

other cancers. The invention provides MTSP20 polypeptides and

chain forms, the nucleic acids encoding them, probes and primers,

expression vectors, host cells, antibodies and transgenic animals.

Nucleic acids encoding MTSP20 or its procease domain can be identificated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (especially systemic vasculitis, scleroderma, pyoderma grangrenosum, vasculopathy, venous, arterial ulcers, Sturge-Weber syndrome, Post-wine stains, blue rubber bleb naevus syndrome, Klippel-Trenaunay-Weber syndrome and Osler-Weber-Rendu syndrome) and ocular disorders (especially blindness caused by ocular neovascular disease, corneal graft neovascularisation, macular degeneration in the eye, neovascular glaucoma, trachoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expressed in a host cell, and the protein used in assays to identify candidate compounds that modulate MTSP activity. A claimed method of inhibiting tumour initiation, growth or progression or for treating a malignant or pre-malignant condition, especially of the breast, cervix, prostate, lung, ovary or colon, involves administering an inhibitor of a MTSP20 polypeptide, especially an antisense oligonucleotide, double-stranded RNA or antibody (all claimed). These inhibitors are also used in a claimed method of treating or preventing a disease or disorder associated with undesired and/or uncontrolled anglogenesis or neovascularisation, especially undesired anglogenesis associated with solid neoplasms,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diabetic retinopathy, myopic degeneration, retinopathy of prematurity, retrolental ribroplasia and corneal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vascular malformations and cardiovascular disorders (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neovascularisation).
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                                                         GGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ
                                                                                                                                                                                                    HR F P F GAS C WATGWD QDTSDA P GTLRNLRLRLISR P T CNCIYNQLHQRHLSN P AR P GMLC
                                                                                                                                                                                                                                                                                                                                                                               WSVVLGSLQREGLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPA
GGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ
                                                                                                                                                       HRFPFGASCWATGWDQDTSDAPGTLRNLRLISRPTCNCIYNQLHQRHLSNPARPGMLC
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98.5%;
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Pred. No. 1.7e
1; Mismatches
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RESULT 8
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The present invention relates to human trypsin designated m32404 proteins and polynucleotides encoding such proteins. m32404 sequences are useful in the prevention, diagnosis and treatment of diseases associated with inappropriate m32404 trypsin expression. They are used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of m32404 trypsin by expressing inactive proteins or to supplement the patients own production of m32404 trypsin. They are also used to prevent, diagnose and/or treat bone disorders (e.g. osteoporosis, osteopenia, tropical sprue), immune disorders (e.g. psoriasis, asthma, allergies), cellular proliferative disorders (e.g. carcinoma, sarcoma and leukaemias), haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding human trypsin m32404, useful for preventing diagnosing and treating e.g. bone disorders, cellular proliferative disorders and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; trypsin; m32404 protein; bone disorder; osteoporosis; osteopenia; tropical sprue; immune disorder; cellular proliferative disorder; asthma; psoriasis; allergy; carcinoma; leukaemia; haematopoietic disorder; psoriasis; allergy; carcinoma; cardiovascular disorder; valvular disease; liver disorder; sarcoma; cardiovascular disorder; valvular disease; arrhythmia; cardiomyopathy; viral disease; pain; metabolic disorder; vaccine; gene therapy; protein therapy; cytostatic; immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
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                                                                                                                                                                                                                                      Human; peptidase; cell proliferative disorder; arteriosclerosis; psoriasis; myelofibrosis; cancer; autoimmune disorder; Crohn's disease; inflammatory disorder; AIDS; anaemia; allergy; asthma; atherosclerosis; Grave's disease; multiple sclerosis; scleroderma; infection; diabetes; metabolic disorder; Addison's disease; cystic fibrosis; diagnosis;
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Pred. No. 1.3e-
26; Mismatches
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RESULT 10
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03-MAY-1999;
27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a human peptidase, designated HPEP-8. The invention relates to 18 human peptidases designated HPEP-1 to HPEP-18, respectively. The peptidases can be used for treating a disease or condition associated with decreased expression or over expression of functional human peptidases. The diseases that can be diagnosed, prevented and treated include cell proliferative disorders (such as arteriosclerosis, psoriasis, myelofibrosis, and cancers), allergies, autoimmune/inflammacory disorders (such as AIDS, anaemia, allergies, Crohn's disease, asthma, atherosclerosis, Grave's disease, multiple sclerosis, and scleroderma), infections, and metabolic disorders (such a Addison's disease, diabetes; cystic fibrosis, glycogen storage diseases
                                      SECP2; secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An isolated polypeptide for diagnosis, prevention cell proliferative, autoimmune/ inflammatory and \pi comprises a sequence encoding a human peptidase -
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                                                                                                                         AAB20156;
                                                                                                                                                   AAB20156 standard; Protein;
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DB; AAA37664.
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                                                                                                                                                                                                                                                                                                                                                     DHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTS 484
                                                                                                                                                                                                                                                                                            AVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVSSLDW
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                                                                   SECP2
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99US-0132253.
99US-0136653.
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99.6%;
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                                        human;
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                                                                                                                                                   267
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Pred. No. 4.8e-93;
0; Mismatches 1
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                                        diagnosis;
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                                        therapy
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metabolic disord
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Matches 264; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of human prostatin precursor. The invention provides 9 novel SECP proteins (see AAB20155-63), nucleic acids encoding them (see AAF30188-96), antibodies, mutants or fragments. These can be used to detect, treat or prevent an SECP-associated disorder, to screen for predisposition to such a disorder, and to identify agents that modulate the expression or activity of SECP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and which does not appear to include a signal peptide. protein shows homology to human PRO351 protein, and to of human prostatin precursor. The invention provides
   Human; transmembrane serine protease 20; MTSP20; enzyme;
endotheliase; cytostatic; dermatological; cardiant; vulnerary;
                                                 Transmembrane serine protease 20
                                                                                                                                            ABP72373 standard; Protein; 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide designated SECP, its encoding nucleic acid and immunospecific antibody, useful for diagnosing, preventing and SECP-associated disorders such as cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUL-1999; 99US-0144722.
29-NOV-1999; 99US-0167785.
19-JUL-2000; 2000US-0619252.
                                                                                 13-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of novel human protein SECP2, which is predicted to localise in the microbody (peroxison
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)B; AAF30189.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       QAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig 2; 124pp;
                                                                                                                                                                                                                                                   QVYFAEEPEPEAEPGSCLANISQPTSC 571
                                                                                                                                                                                                                                                                                                               AVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVSSLDW
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                                                                              (first entry)
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Pred. No. 8.4e-92;
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                                              (MTSP20) protease domain
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protein (endotheliase) that is expressed in osophageal tumour tissues, in lung carcinoma, colon, cervix, leukaemia and other cell lines as well as in certain healthy cells and tissues. The level of MTSP20 can be diagnostic of prostate, uterine, lung, coesophagus or colon cancer, or leukaemia. The expression and/or activation of MTSP20 on, or in the vicinity of, a cell.or a bodily fluid can be a marker for breast, prostate, lung, colon and other cancers. The invention provides MTSP20 onlypeptides and other cancers. The invention provides MTSP20 polypeptides and primers, chain forms, the nucleic acids encoding them, probes and primers, chain forms, the nucleic acids encoding them, probes and primers, expression vectors, host cells, antibodies and transgenic animals. Nucleic acids encoding MTSP20 or its protease domain can be expressed in a host cell, and the protein used in assays to identify candidate compounds that modulate MTSP activity. A claimed method
                         haemophiliac joints, inflammatory bowel disease, nonhealing fractures, periodontitis, psoriasis, rheumatoid arthritis, venous stasis ulcers, granulations-burns, hypertrophic scars, liver cirrhosis, osteoradionecrosis, postoperative adhesions, pyogenic granuloma and systemic sclerosis) aberrant wound repairs, circulatory disorders (especially Raynaud's phenomenon) crest syndromes (especially calcinosis, oesophageal, dyomotiloty, sclerodactyly and telangiectasis), dermatological disorders (especially systemic vasculitis, scleroderma, pyoderma (especially systemic vasculitis, scleroderma, pyoderma grangrenosum, vasculopathy, venous, arterial ulcers, Sturge-Weber syndrome, Post-wine stains, blue rubber bleb naevus syndrome, and ocular disorders (especially blindness caused by ocular neovascular disease, corneal graft neovascularisation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of inhibiting tumour initiation, growth or progression or for treating a malignant or pre-malignant condition, especially of the breast, cervix, prostate, lung, overy or colon, involves administering an inhibitor of a MTSP20 polypeptide, especially an antisense oligonucleotide, double-stranded RNA or antibody (all claimed). These inhibitors are also used in a claimed method of treating or preventing a disease or disorder associated with undesired and/or uncontrolled angiogenesis or neovascularisation, especially undesired angiogenesis associated with solid neoplasms, vascular malformations and cardiovascular disorders (especially angiofibroma, angiolipoma, atherosclerosis, restenosis/reperfusion in the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adhesion, dyschondroplasia with vascular hamartoma (Fafucci's syndrome), hereditary haemorrhagic telangiectasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New type-II membrane-type serine protease 20 polypeptides, useful for preparing a medicament for diagnosing, treating or preventing cancer, dermatological disorders, aberrant wound repairs or crest syndromes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  syndrome), hereditary haemorrhagic telangiectasia (Rendu-Osler-Weber syndrome) and von Hipple Lindau syndrome), chronic inflammatory diseases (especially diabetes mellitus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              injury, arteriovenous malformations, haemangiomatosis and vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              novel
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                      The present sequence is that of novel human protein SECP8, which is predicted to localise in the cytoplasm, and which does not appear to include a signal peptide. The invention provides novel SECP proteins (see AAB20155-63), nucleic acids encoding the protein of the protein o
                                                                                                                                                                                                                    Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protease #6 encoded by clone HTTJK57.
                                                                           2000WO-US12207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
99US-0133239.
99US-0135163.
99US-0147005.
99US-0152935.
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                                                                                                                                                                            /note=
/202
                                                                                                                                                                                                                                             /label= Histidine_active_site_domain 115..123
                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                 158..167
                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                          /note=
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                                                                                                                                                                                                                                                                                          "Immunogenic epitope"
                                                                                                                                                                  "Immunogenic epitope"
                                                                                                                                                                                               "Immunogenic
                                                                                                                                                                                                                             "Immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1023; D
Pred. No. 2.6e
0; Mismatches
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No. 2.6e-63;
                                                                                                                                                                                                                             epitope"
                                                                                                                                                                                               epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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99US-0162979

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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC disorders (osteoporosis), connective tissue disorders (arthritis), altoimmune disorders (systemic lupus erythematosus), wound healing, male creproductive system disorders (testicular cancer), digestion and food absorption disorders (Crobn's disease), neurodegenerative diseases (Crobn's disease), neurodegenerative diseases (Alzheimer's disease), behavioral disorders (Tourette's syndrome), CC proliferative and cancerous conditions (acute myelogenous leukaemia), CC cocular disorders (glaucoma) and infectious diseases caused by bacteria, CC viruses, fungi or parasites. It is also useful for screening therapeutic compounds. Serine proteases are used as immunological probes or CC compounds. Serine proteases are used as immunological probes or CC compounds in biological samples, identification of chromosomes, cells and CC tissues in biological samples, identification of male contraceptive CC agents, delivery of compositions to targetted cells expressing a CC receptor for serine protease nucleic acids are also useful in gene therapy. CC Note: The present sequence shown in page 282-283 of sequence listing has been assigned SEQ ID NO: 16. But the sequence, peptide fragment #14 CC related to human serine protease (AAY72117) shown in page 15 is also contact.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Si
Matches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid molecules encoding human serine protease polypeptides, useful for diagnosis, prevention and/or treatment of disorders e.g. osteoporosis, lupus erythematosus and Alzheimer's -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTTUK57 (ATCC Deposit No: PTA538).

The invention relates to human serine proteases and their cDNA clones
It is used in methods for the diagnosis, prevention and treatment of
various disorders related to serine protease such as bone formation
                      Amino acid sequence of a human
                                                       26-NOV-2001
                                                                                                                            AAG67515 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                     27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                           GGPQPGVQGPCQ 239
                                                                                                                                                                                                                                                                                                                                                                                   WSVVLGSLQREGLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPA
                                                                                                                                                                                                                                                                                                              HREPEGASCWATGWDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLC
                                                                                                                                                                                                                                                                                                                                                             WSVVLGSLQREGLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPA
                                                                                                                                                                                                                                                                                                                                                                                                                                   QRGPGPPKPQEGNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           QEPQGKAK-RHGNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNS
                                                                                                                                                                                                                     GGPQPGVQGPCQ 218
                                                                                                                                                                                                                                                                                          HRFPFGASCWATGWDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.3%;
ilarity 95.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence is human serine protease
                                                     (first entry)
                                                                                                                            Protein; 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1003.5;
Pred. No. 6.5e
1; Mismatches
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RFPFGASCWATGWDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCG RFPFGASCWATGWDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCG VGAFCARRRGPGFWLESETFPVAVYLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAH LGSLQREGLSPG---AEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAH 168

198 228 138

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                                                                                                                                          The present sequence represents a human secreted polypeptide. The secreted polypeptides and polymelectides are useful for treating nervous and muscular diseases, for inhibiting tumour formation and treatstasis, for treating gastrointestinal ulceration, for preventing and treating diseases in spinal cord, thyroid gland, ovary, prostate, renal gland, small intestine, heart, trachea, thymus, lymph node, muscular system and colon, for treating lipase deficiency in cystic fibrosis and pancreatitis, for treating undesirable clot formation so that require decreased blood clot formation, for treating procedures that require decreased blood clot formation, for treating limune disorders and microbial diseases, for treating immune disorders, for treating inflammation and transplant rejection, for enhancing bone thickness and increasing bone density, and for regulating vascular smooth cell proliferation. They
                                                                   Query Match
Best Local Sim
Matches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted polypeptide; nervous disease; muscular disease; tumour; gastrointestinal ulceration; spinal cord disease; trachea disease; thyroid gland disease; ovary disease; prostate disease; heart disease; renal gland disease; small intestine disease; thymus disease; lymph node disease; muscular system disease; colon disease; lipase deficiency; cystic fibrosis; pancreatitis; clot formation; myocardial infarction; angiopolasty; liver disease; coagulation disorder, microbial disease; immune disorder; inflammation; transplant rejection; bone thickness; bone density; ferroxidase loss; apoptosis; vascular smooth cell proliferation; vaccine.
                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated secreted polypeptide useful for treating nervous and muscular diseases, gastrointestinal ulceration, coagulation and immune disorders, microbial diseases, inflammation and transplant rejection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agarwal P, Murdoch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK )
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03-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Page 74-75; 102pp; English
                                53
24 GKAPR-----PGAWPWEAQVMVPGSRPCHGALVSESWVLAPASCFLEQVTHTLCCCRMTR 78
                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMITHKLINE BEECHAM CORP SMITHKLINE BEECHAM PLC.
                              GKAKRHGNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCF-EKAAATELNSWSVV
                                                                                                                                                                          be used as
                                                                                                                                          301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; 2000US-0187107.
; 2000US-0188916.
; 2000US-0236874.
; 2000US-0237846.
                                                                     Conservative
                                                                                                                                          A
A
                                                                                                                                                                       regulating vascular smooth cell proliferation. They succines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR,
                                                                                 28.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rizvi SK,
                                                                     10;
                                                                                   Score 896.5; DB 2
Pred. No. 2.4e-54;
                                                                     Mismatches
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                                                                                                     DB 22;
                                                                     44;
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                                                                      Indels
                                                                                                       Length
                                                                     267;
                                                                                                       301;
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RESULT 15
AAG67514
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                                                                                                                                                                                            13-MAR-2000;
03-OCT-2000;
03-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted polypeptide; nervous disease; muscular disease; tumour; gastrointestinal ulceration; spinal cord disease; trachea disease; thyroid gland disease; ovary disease; prostate disease; heart disease; renal gland disease; small intestine disease; thymus disease; lymph node disease; muscular system disease; colon disease;
                               Novel isolated secreted polypeptide useful for treating nervous and muscular diseases, gastrointestinal ulceration, coagulation and immune disorders, microbial diseases, inflammation and transplant rejection -
                                                                                                                                                                                                                                                                                                                                                                            lipase deficiency; cystic fibrosis; pancreatitis; clot formation; myocardial infarction; angioplasty; liver disease; coagulation disorder; microbial disease; immune disorder; inflammation; transplant rejection; bone thickness; bone density; ferroxidase loss; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a human secreted polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG67514 standard;
        Claim 1; Page
                                                                                       N-PSDB;
                                                                                                                                                                                                                                  06-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                  vascular
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                                                                                                                             ש
                                                                                                                                                      SMITHKLINE SMITHKLINE
                                                                                       AAH78206
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||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTALPAYEDWVSSLDW--QVYFAEEPEPEAEPGSCLANIS 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGGDGSPILPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAV 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVQGAAFLAQSPETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGAL
                                                                                                                                                                                                                                                                                                                                                                    smooth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVTLGASLRPLCLPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAA
                                                                                                                                                                                            ; 2000US-0187107.
; 2000US-0188916.
; 2000US-0236874.
; 2000US-0237846.
                                                                                                                            Murdoch
                                                                                                                                                                                                                                                            2001WO-US07143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
         73-74; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                  cell
                                                                                                                                                      BEECHAM CORP
BEECHAM PLC.
                                                                                                                          PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                  proliferation; vaccine
                                                                                                                            Rizvi SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255
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                                                                                                                             Smith
                                                                                                                          Xiang
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The present sequence represents a human secreted polypeptide. The secreted polypeptides and polymcleotides are useful for treating CC nervous and muscular diseases, for inhibiting tumour formation and CC metastasis, for treating gastrointestinal ulceration, for preventing CC and treating diseases in spinal cord, thyroid gland, ovary, prostate, CC muscular system and colon, for treating lipase deficiency in cystic CC fibrosis and pancreatitis, for treating undesirable clot formation CC such as mycardial infarction, during angioplasty and all surgical CC procedures that require decreased blood clot formation, for treating CC liver diseases, coagulation disorders and microbial diseases, for treating inflammation and transplant CC rejection, for enhancing bone thickness and increasing bone density, CC for reducing the loss of essential ferroxidases, for suppressing contraction and transplant contractions and for requilating vascular smooth cell proliferation. They
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A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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A Stapleton M., J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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A Whiting M., Wadan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Hulkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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Q16651; Q9UCA3;
Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
The procursor (EC 3.4.21.-).
MEDILING=973000., Yu J.X., Chao J., Yu J.X., Chao L., Chao J., "Prostasin is a novel human serine proteinase from s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22388257; PubMed=12477932;
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Mammalia; Eutheria;
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                                                                                                          SEQUENCE OF 45-64.
                                                                                                                                              "Generation and initial analysis of more human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-10
                                                                   MEDLINE=94308140;
                                                                                          TISSUE-Semen;
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J. Biol. Chem. 270:13483-13489(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95286644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 NTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chao L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CWATGW----DQDTSDAPGTLRNLRLRLISRPTCNCIYNQ-----LHQRHLSNPARPGML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGPHAMYARVRQVESNPLYQGTASSADVALVELEAPVPFTNYILPVCLPDPSVIFETGMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DTQEGEWPWQVSIQRNGSHFCGGSLIAEQWVLTAAHCFRNTSETSL--YQVLLGARQLVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGFEEGKKDACKGDSGGPLVCLVGQS-WLQAGVISWGEGCARQNRPGVYIRVTAHHNWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLINTAAHSSWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CWVTGWGSPSEEDLLPEPRILQKLAVPIIDTPKCNLLYSKDTEFGYQPKTIKN----DML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chao J.;
                                                                     PubMed=8034638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=7768952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; (
Primates; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 449; DB 1;
Pred. No. 4.6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                              99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                   than 15,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                               seminal fluid
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           prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157
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Matches
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J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005615; C:extracellular space; GO; GO:0005886; C:plasma membrane; TAS InterPro; IPR001314; Chymotrypsin. InterPro; IPR001254; Ser protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; S01.159; --
Genew; HGNC:9491; PRSS8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L41351; AAC41759.1; -.
EMBL; U33446; AAB19071.1; -.
EMBL; BC001462; AAH01462.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A57014; A57014.
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: HETERODIMER
                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: FOUND IN PROSTATE, LIVER, SALIVARY GLAND, KIDNEY, LUNG, PANCREAS, COLON, BRONCHUS AND RENAL PROXIMAL TUBULAR CELLS. IN THE PROSTATE GLAND IT MAY BE SYNTHESIZED IN EPITHELIAL CELLS, SECRETED INTO THE DUCTS, AND EXCRETED INTO THE SEMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. Chem. 269:18843-18848(1994).
FUNCTION: POSSESSES A TRYPSIN-LIKE CLEAVAGE SPECIFICITY
SUBUNIT: HETERODIMER OF TWO CHAINS, LIGHT AND HEAVY, HE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: MEMBRANE-BOUND. ITS C-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          600823;
                                                                       111
                                    99
                                                                                                             41
                                                                                                                                                51
                                                                                                                                                                                                      Similarity
                                                                       VLGSLQREGLSPGAEEVGVAALQ--LPRAYNHYSQGS--DLALLQLAHPTTHT----PLC
                                                                                                                                    PQGKAKRHGNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSV 110
                                                                                                             POARITGGSSAVAGOWPWOVSITYEGVHVCGGSLVSEOWVLSAAHCFPSEHHKE--AYEV
                                                                                                                                                                                                                                                            Serine
                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                              ΑA;
                                                                                                                                                                                                                                                                                                 244
223
262
262
134
238
                                                                                                                                                                                                                                                                36431
                                                                                                                                                                                                        14.1%;
35.3%;
                                    -EDAKVSTLKDIIPHP-SYLQEGSQGDIALLQLSRPITFSRYIRPIC
                                                                                                                                                                                                                                                                MW.
                                                                                                                                                                                       48;
                                                                                                                                                                                                                                                        POTENTIAL.
SERINE PROTEASE.
SERINE PROTEASE.
INTERCHAIN (BY SIMILARITY)
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
N-LINKED (GLUNAC. . .) (POTMIC, POTMIC, POTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zymogen;
                                                                                                                                                                                     Score 437.5; DB 1
Pred. No. 3.2e-22;
8; Mismatches 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVATION PEPTIDE.
PROSTATIN LIGHT CHAIN
PROSTATIN HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECRETED AFTER CLEAVAGE
                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                       109;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
                                                                                                                                                                                       Indels
                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                 (POTENTIAL)
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                                                                                                                                                                                   Gaps
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                                      154
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LPQPAHRFPFGASCWATGWDQDTSD----APGTLRNLRLRLISRPTCNCIYNQLHQRHLS

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A COCOCARRARARARA COCOCACACA COCACARRARA COCOCACA COCACA C
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAT
                                                                                                          Pfam; PF00089; trypsin; T.

PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp_Sec; 1.

PROSITE; PSS0240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
   CHAIN
CHAIN
PROPEP
                                                                                                                                                                                                                                       EMBL; AB017638; BAB20281.1; -. EMBL; AF202076; AAG32641.1; -. HSSP; P00734; 1UVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adachi M., Kitamura
Submitted (SEP-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSS8 RAT
Q9ES87; Q9ER01;
                                                                SIGNAL
                                                                                                Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                  PROPEP
                                                                                                                                                                                                   InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                ransmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [SSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFIDE BOND (BY SIMILARITY).
SUBCELLULAR LOCATION: MEMBRANE-BOUND. SECRETED
ITS C-TERMINUS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HETERODIMER OF TWO CHAINS, LIGHT AND HEAVY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: POSSESSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a cent the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLGLALGLLSPW 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAGPQAGAPSPW 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASSYASWIQSKVTELQPRVV----PQTQE-SQPDSNL-CGSHLAFSSAPAQGLLRPILFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAHSSWLQARV---QGAAFLAQSPETPEMSDEDSCVACGS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HFVQEDMVCAGYVEGGKDACQGDSGGPLSC-PVEGLWYLTGIVSWGDACGARNRPGVYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NPARPGMLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPAANASFPNGLHCTVTGWGHVAPSVSLLTPKPLQQLEVPLISRETCNCLYNIDAKPEEP
                                                                                                                                                                                                                                                                                                                                                    non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               c cloning and expression of rat prostasin.";
(NOV-1999) to the EMBL/GenBank/DDBJ databas
ION: POSSESSES A TRYPSIN-LIKE CLEAVAGE SPECI
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                                                                                               protease;
   322
342
342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miyoshi T., Tomita K., the EMBL/GenBank/DDBJ
                                                                                             Zymogen; Signal; Glycoprotein;
POTENTIAL.

ACTIVATION PEPTIDE (BY SIMILARITY)

PROSTATIN LIGHT CHAIN.

PROSTATIN HEAVY CHAIN.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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   RESULT 4
BSS4_MOUSE
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16-OCT-2001
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                               EMBL; AB010778; BAB20262.1; HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                      TISSUE=Brain;
Mitsui S., Okui A.,
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                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
   MGI:1918085;
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   4733401N09Rik.
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Brain-specific serine protease 4 precursor (EMPRSS22 OR PRSS26 OR BSSP4.

Sukarran (Mouse)
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                          Mitsui S., Okui A., Kominami K., Yamaguchi N.; "Cloning and characterization of a novel serine Submitted (JAN-1998) to the EMBL/GenBank/DDBJ da-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKGGKDACQGDSGGPLSC-PIDGLWYLAGIVSWGDACGAPNRPGVYTLTSTYASWIHHHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HCTVTGWGHVAPSVSLQTPRPLQQLEVPLISRETCSCLYNINAVPEEPHTIQQDMLCAGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGA
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CHARGE RELAY SYSTEM
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Pred. No. 3.4e-21;
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A -> V (IN REF. 1).
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SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleosto
Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 AA
                                                                    There are no restricting as its content is
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                        http://www.isb-sib.
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                                                                                                                                                                                                   databases
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(BY SIMILARITY).
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                                                                                                               EMBL
                                                                                                                                                                                                                         mBSSP-4.";
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                                                                                                                                 a collaboration
                                                 for
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                             .ch/announce/
                                                                                                               outstation
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PSS8 MOUSE
ID PSS8 MOUSE
AC 09ESD1;
DT 16-0CT-2001
DT 16-0CT-2003
CRRRRRRR ROCCONDITION
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Best Local S
Matches 106
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PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM00020; Tryp SPC; 1.

PROSITE; PS00134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN SER; 1.

Hydrolase; Serine protease; Signal
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DISULFID
CARBOHYD
SEQUENCE
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ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
DISULFID
                                                                                                                                                                                Prostasin precurse-
PRSS8 OR CAP1.
                       MEDLINE=20235202; PubMed=10770960; Vuagniaux G., Vallet V., Jaeger N.F., P
Courtois-Coutry N., Vandewalle A., Ross
"Activation of the amiloride-sensitive
the serine protease mCAP1 expressed in
duct cell line.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                J. Am.
                                                                                                                                         Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
InterPro;
                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                       Eukaryota; Metazoa;
 FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                289
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                Soc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGAEEVGVAALQLPRAYNHYSQG--SDLALLQLAHPTTHT----PLCLPQPAHRFPFGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGNTVPGE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CWIAGWGSIQDGVPLPHPQTLQKLKVPIIDSELCKSLY----WRGAGQEAITEGMLCAGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CWATGW----DQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPA-RPGMLCGGP
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IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine protease; Signal
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                                                                                                                                                                                            (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
(Recursor (EC 3.4.21.-) (Channel activating
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90
141
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238
              Nephrol.
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 POSSESSES
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                                                                                                                                                                                                                                                                                           STANDARD;
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141
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                                                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33262
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33.7%;
              11:828-834 (2000)
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V
TRYPSIN-LIKE
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
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Pred.
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                                                                                                                                                                       Craniata; Vertebrata;
                                                                                                                                                          Sciurognathi;
                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            417;
                                         F., Pfister C., Bens M.
Rossier B.C., Hummler
tive epithelial sodium
d in a mouse cortical c
                                                                                                                                                                                                                                                                                         342
CLEAVAGE
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5.5e-21;
les 114;
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SPECIFICITY
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                                      M., Farman N
or E.;
or E.)
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Best Local
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PFEAM: PF000722; CHYPPLESS SMART; SM00020; Tryp SPc; 1.

SMART; SM00020; Tryp SPc; 1.

PROSITE; PS50240; TRYPSIN DOM; 1.

POSITE; PS00134; TRYPSIN SER; 1.

PS0135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                           Matches
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SEQUENCE
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DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
ACT_SITE
ACT_SITE
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PROPEP
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PROPEP
CHAIN
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InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; I.
PRINTS; PR00722; CHYMOTRYPSIN.
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HSSP; P00734; 10
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                            286
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 AELQPRV---
                            --LOARVOGAAFLAQSPETPE
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244
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SIMILARITY). ACTIVATES AMILORIDE-SENSITIVE SUBUNIT: HETERODIMER OF TWO CHAINS, LIGHT A DISULFIDE BOND (BY SIMILARITY). SUBCELLULAR LOCATION: MEMBRANE-BOUND. SECRE ITS C-TERMINUS (BY SIMILARITY). BELONGS TO PEPTIDASE FAMILY SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY:
CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT
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AND HEAVY, HELD 1
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(See http://www.isb-sib.ch/announce/ restrictions and EMBL a collaboration - MBL outstation -18 ä ö

Signal; Glycoprotein; SIMILARITY).

BY SIMILARITY.
BY SIM SERINE PROTEASE INTERCHAIN (BY S ACTIVATION PEPTIDE (BY PROSTATIN LIGHT CHAIN. PROSTATIN HEAVY CHAIN. BY SIMILARITY. -LINKED (GLCNAC... -LINKED (GLCNAC... 0620DE88ED187D0F DB 1; L.2e-20; 102; SIMILARITY) Length CRC64 (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(POTENTIAL). Indels (POTENTIAL) 342; 26; Gaps 9

QPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSW-----SCWATGW----DQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGP HCTVTGWGHVAPSVSLQTPRPLQQLEVPLISRETCSCLYNINAVPEEPHTIQQDMLCAGY SYSNDTVVHTVAQIITHSSYREEGSQGDIAFIRLSSPVTFSRYIRPICLPAANASFPNGL GLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGA GSAKPGQWPWQVSITYDGNHVCGGSLVSNKWVVSAAHCFPREHSRE--AYEVKLGAHQLD GNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQRE VKGGKDACQGDSGGPLSC-PMEGIWYLAGIVSWGDACGAPNRPGVYTLTSTYASWIHHHV 174 166 106 285 230 226

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Bitterenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Raha S.S., Korley K.C., Hale S., Garcia A.M., Gay L.J., Hulk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha Hakesley R.W., Touchman J.W., Madan A., Rodrigues S., Sanchez A.,

Raha Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Raha Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Raha Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9GZN4; O43342;
16-OCT-2001 (Rel. 40, C
16-OCT-2001 (Rel. 40, I
15-SEP-2003 (Rel. 42, I
Brain-specific serine K
                                                                                                                                                                                                          Ricke D.O., Bruce D., Mundt M., Doggett N., Munk C., Saunder Robinson D., Jones M., Buckingham J., Chasteen L., Thompson Goodwin L., Bryant J., Tesmer J., Meincke L., Longmire J., Veng S., Tatum O., Campbell C., Fawcett J., Deaven L.; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SP001LA).
PRSS22 OR PRSS26 OR BSSP4.
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                                                               modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                               SEQUENCE OF 47-317 FROM N.A.
Ricke D.O., Bruce D., Mundt M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22388257;
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"Identification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Pancreas;
Wong G.W., Steve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and characterization protease, hBSSP-4.";
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                                                  or send an
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              AB010779;
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Eutheria; Primates;
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                                                email to license@isb-sib.ch).
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             BAB20263.1;
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Last annotation update)
protease 4 precursor (EC 3.4.21.-)
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                                                                 (See http://www.isb-sib.ch/announce/
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RESULT 7
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IN CONTROL

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DT 16-0
DT 16-0
DT TYP
GN TPSG
GN HOMO
OC BUKA
OC MAMM
OX NCBII
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TRYG HUMAN STANDARD;
TRYG HUMAN STANDARD;
Q9NRR2; Q9C015; Q9NRQ8; Q9UBB2;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
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ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
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CONFLICT
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                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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ACT_S
ACT_S
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PROSITE; PSS00134; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
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EMBL; AC003965;
SEQUENCE FROM N.A. (VARIANTS GAMMA-1 AND GAMMA-2)
MEDLINE=20302813; PubMed=10843716;
Caughey G.H., Raymond W.W., Blount J.L., Hau L.W.
                                                                                                       Tryptase gamma precursor TPSG1 OR TMT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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InterPro; IPR001254; Ser_protease_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS; S01.252; -.
Genew; HGNC:14368; PRSS22
                                                                                         Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                 SDAPGTLRNLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGP
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                                                                                                                                                                                                                                                   -----GGGALRAPSQGSGA 313
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227
266
266
47
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317
90
141
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91
                                                               Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33731 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.9%;
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L -> M (IN REF. 4).
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Pred. No. 9.1e-20;
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                                                               Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E2A123BC86E79935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                  update)
(Transmembrane tryptase)
 Hau L.W.,
                                                                  Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 317;
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  Pallaoro
                                                                              Euteleostomi;
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EMBL; AF191031; AAF76457.1; -
EMBL; AF195508; AAF76458.1; -
EMBL; AF175759; AAF703697.1; -
EMBL; AF775522; AAF703695.1; -
EMBL; AF223563; AAG48852.2; -
HSSP; P00763; IDPO.
                                                                                                                                          DISULFID
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CHAIN
TRANSMEM
ACT_SITE
ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99452974; PubMed=10521469; Wong G.W., Tang Y., Feyfant E., Sali A., Li L., Friend D.S., Krilis S.A., Stevens R.L.; "Identification of a new member of the tryptase human mast cell proteases which possesses a nove hydrophobic extension.";
CONFLICT
                                                                                                                                                                                                                                                  Transmembrane;
SIGNAL
                                                                                                                                                                                                                                                                                          PROSITE; PS50240;
PROSITE; PS00134;
                                                                                                                                                                                                                                                                                                               Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                      VARIANT
                                           VARIANT
                                                                                     VARIANT
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                                                                                                                       CARBOHYD
                                                                                                                               DISULFID
                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                        Hydrolase;
                                                                                                                                                                                                                                                                                 PROSITE; PS00135;
                                                                                                                                                                                                                                                                                                                             InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam: PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:14134; TPSG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Organization and alternative splicing of CACNAIH."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: MEMBRANE-ANCHORED (Potential).
TISSUE SPECIFICITY: Expressed in many tissues.
POLYMORPHISM: There are two alleles; gamma-I and gamma-II which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration meen the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
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ization of human gamma-tryptases, nove
16p mast cell tryptase and prostasin
. 164:6566-6575(2000).
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215
215
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TRYPSIN_HIS; 1.
TRYPSIN_SER; FALSE_NEG.
protease; Signal; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                             Lymorphism
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321
304
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228
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TRYPTASE GAMMA HEAVY CHI
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INTERCHAIN (POTENTIAL).
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        L -> I (IN GAMMA-)
/FTId=VAR 012100.
L -> F (IN GAMMA-)
/FTId=VAR 012101.
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S
                                     VAR 012099.
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(See http://www.isb-sib.ch/announce/
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Widin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Widin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Widin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Widin T.B., Toshiyuki S., Carninci P., Willahy S.J.,
RA Roberts S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. TISSUE=Liver; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                  Brathwaite M., Waeltz P.,
Nagaraja R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91184812; PubMed=
Degen S.J., Bell S.M., Sc
"Characterization of the
localization of the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P20918; Q8CIS2; Q91WJ5;
01-FEB-1991 (Rel. 17, C
15-SEP-2003 (Rel. 42, L
15-SEP-2003 (Rel. 42, L
                                                                                                                                                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129/Sv;
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasminogen precursor
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                                                                                                                                                                                                                                                                                                                                      sequence analysis in the mouse t-complex region."; i (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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35.5%;
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Last annotation update)
(EC 3.4.21.7) [Contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schaefer L.A., Elliott ne cDNA coding for mous ne to mouse chromosome
                                                                                                                                                                                                                                                                                                                                                                                    Qian Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 382; DB 1;
Pred. No. 1.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; I
Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                    Dudekula D.,
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for mouse plasminogen
romosome 17.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murinae;
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MEROPS; S01.233; 1.

MGD; MGI:97620; P19.

GO; GO:0016506; F:apoptosis activator ac

GO; GO:0006915; P:apoptosis; IDA.

InterPro; IPR001314; Chymotrypsin.

InterPro; IPR003001; Kringle.

InterPro; IPR003014; pAN.

InterPro; IPR003609; Pan app.

InterPro; IPR003609; Pan app.

InterPro; IPR003966; Prothrombin.

InterPro; IPR003966; Prothrombin.

InterPro; IPR0031254; Ser protease_Try.

Pfam; PF00051; kringle; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC014//3, AAN EMBL; AY134430; AAN PIR; A38514; PLMS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parmer R.J., Miles L.A.;
"Localization of regulatory elements recytokine-stimulated plasminogen gene cytokine-stimulated plasminogen gene J. Biol. Chem. 277:38579-38588(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J04766; AAA50168.1; -. EMBL; AF481053; AAM22156.1; -. EMBL; BC014773; AAH14773.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
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ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN ACTIVATORS, BOTH PLASMINOCEN AND ITS ACTIVATOR BEING BOUND TO FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.

MISCELLANBOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.

MISCELLANBOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION INVOLVES ONLY CLEAVAGE AFTER ARG-581, RESULTING IN 2 CHAINS HELD TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PERFIDE.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY SIMILARITY: Contains 5 kringle domains.
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FUNCTION: ANGIOSTATIN IS AN ANGIOGENESIS INHIBITOR THAT BLOCKS NEOVASCULARIZATION AND GROWTH OF EXPERIMENTAL PRIMARY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse cDNA sequences."
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CATALYTIC ACTIVITY: Preferential higher selectivity than trypsin.
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.J.M., Marra M.A.;
of more than 15,000 full-length
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Converts fibrin into soluble
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SMART; SM00130; KR; 5.

$ SMART; SM00473; PAN_AP; 1.

$ SMART; SM00473; PAN_AP; 1.

$ R SMART; SM00020; Tryp_SPc; 1.

$ R SMART; SM00021; KRINGLE 1; 5.

$ R PROSITE; PS500021, KRINGLE 2; 5.

$ PROSITE; PS500134; TRYPSIN_DOM; 1.

$ PROSITE; PS00134; TRYPSIN_HIS; 1.

$ PROSITE; PS00135; TRYPSIN_SER; 1.

$ PROSITE; PS00136; TRYPSIN_SER; 1.

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PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
PRINTS; PR01505; PROTHROMBIN.
ProDom; PD000395; Kringle; 5.
SMART; SM00130; KR; 5.
SMART; SM00473; PAN AP; 1.
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PF00089;
                                                                                   551
                                          76
                                                                                                                              23
                                                                                                                                                                                             Similarity
                                                                                   --GAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQ
FTGQHFCGGTLIAPEWVLTAAHCLEKSSRPEF--YKVILGAHEEYIRGSDVQEISVAKLI
                                                                                                                                                                                                                                                        235
525
649
812
                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                          ΑA;
                                                                                                                                                                                                                                                                                                                                                                    90781 MW;
                                                                                                                                                                                           12.0%;
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CHARGE RELAY SYSTEM (
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EXAMPLE OF THE STATE 
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INTERCHAIN (BY S
BY SIMILARITY.
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PLASMIN LIGH
KRINGLE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRINGLE 4.
                                                                                                                                                                      Score 371.5; DB
Pred. No. 2e-17;
5; Mismatches 1(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRINGLE
KRINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTIVATION PEPTIDE.
PLASMIN SHORT FORM OF CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLASMINOGEN
PLASMIN HEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRINGLE
                                                                                                                                                                                                                                                            7 -> H (IN REF. 1).
7 -> D (IN REF. 1).
8 -> L (IN REF. 1).
7 -> L (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIGHT CHAIN B
                                                                                                                                                                         107;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                              CRC64;
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(BY SIMILARITY).
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                                                                                                                                                                         Indels
                                                                                                                                                                                                               Length
                                                                                                                                                                                                                 812;
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                                                                                                                                                                         39;
                                                                                                                                                                         Gaps
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                                                                                     602
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PLMN P
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WMEDLINGE-BRIBSJ29; PubMed=3356193;

WA MARTIT., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,

RA Gerwig G.J., van Halbeek H., Vilegenthart J.F.;

RA GERwig G.J., van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
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P06867;
01-JAN-1988
01-FEB-1991
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-560.
Schaller J., Marti T., Roesselet S.J., Pamino acid sequence of the heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                             <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             miniplasminogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-85203907; PubMed=3846533;
Marti T., Schaller J., Rickli E.E.;
"Determination of the complete amino-acid sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the carbohydrate attachment species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYDRATE-LINKAGE SITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 450-790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ibrinolysis 1:91-102(1987).
                  (MICROHETEROGENEITY).

MISCELLANEOUS: PLASMIN IS INACTIVATED BY IMMEDIATELY AFTER DISSOCIATION FROM THE C SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: Contains 5 kringle domains.
                                                                                                                                             Products.

ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN ENZYME REGULATION: CONVERTED AND ITS ACTIVATOR BEING BOUND ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.

PTM: N-LINKED GLYCAN CONTAINS N-ACETYLLACTOSAMINE, SIALIC A IS CORE FUCCOSYLATED. O-LINKED GLYCANS CONSIST OF GAL-GALMAC DISACCHARIDE WITH IS MODIFIED WITH UP TO 2 SIALIC ACID RESI
                                                                                                                                                                                                                                                                                                                           ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSS LANDININ AND VON WILLLEBRAND FACTOR.

CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-xaa > higher selectivity than trypsin. Converts fibrin into s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. 149:279-285(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CFEKDKYILQ-GVTSWGLGCARPNKPGVYVRVSRFVDWIEREMR
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17, Last sequence update)
41, Last annotation update)
.4.21.7).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                et S.J., Kaempfer U., Rickli E. avy chain of porcine plasmin. C sites with the human and bovir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -EYLNNRVKSTELCAGQLAGGVDSCQGDSGGPLV
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                                                 S1.
                                                                                                 ALPHA-2-ANTIPLASMIN
                                               PLASMINOGEN SUBFAMILY
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                                                                                                                                                                                                                                                                                                                             -Xaa > Arg-|-:
into soluble
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                                                                                                                                                                                                    SIALIC ACID AND
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RESULT 10
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DT 16-00

MOUSE STANDARD; TEST MOUSE STANDARD; OSUHJ7; OSDA14; 16-OCT-2001 (Rel. 40, Created)

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Best Local :
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InterPro; IPR00356; ProEhrombin.
InterPro; IPR00356; ProEhrombin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00051; kringle; 5.
Pfam; PF00024; PAN; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
PRINTS; PR000195; PROTHROMBIN.
PROBINTS; PR0105; PROTHROMBIN.
PROBITS; PR000130; KR; 5.
SMART; SM00130; KR; 5.
SMART; SM00130; KR; 5.
SMART; SM00201; KRINGLE_1; 5.
PROSITE; PS00021; KRINGLE_1; 5.
PROSITE; PS00021; KRINGLE_2; 5.
PROSITE; PS000134; TRYPSIN_HIS; PALSE_NEG.
PROSITE; PS00134; TRYPSIN_HIS; PALSE_NEG.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000001; Kringle.
InterPro; IPR003014; PAN.
InterPro; IPR003609; Pan app.
InterPro; IPR003609; Prothrombin.
InterPro; IPR001254; Ser protease_Tr
Pfam; PF00051; kringle; 5.
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue remodeling;
CHAIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase;
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747
                                           249
                                                                                           693
                                                                                                                                      189
                                                                                                                                                                                    638
                                                                                                                                                                                                                                 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                     LFDYCDVPQCVTS-----SFDCGKPKVEPKKCPARVVGGCVSIPHSWPWQISLRY
                                           LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ
                                                                                           AGLLKEARLPVIENKVCN-----RYEYLGGKVSPNELCAGHLAGGIDSCQGDSGGPLVC
                                                                                                                                      PGTLRNLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLC
                                                                                                                                                                                    ----FKEPSE-ADIALLKLSSPAVITDKVIPACLPTPNYVVADRTACYITGWGETKGTYG
                                                                                                                                                                                                                             LPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGWDQDTSD-A
                                                                                                                                                                                                                                                                               RYRGHFCGGTLISPEWVLTAKHCLEKSSSP--SSYKVILGAHEEYHLGEGVQEIDVSKL-
                                                                                                                                                                                                                                                                                                                     ROGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQ
                                                                                                                                                                                                                                                                                                                                                                                                                 LYDFCIV--CITTYAINVSLMWLSF----RKVQEPQGKAKRHGN--TVPGEWPWQASVR-
FEKDKYILQ-GVTSWGLGCALPNKPGVYVRVSRFVTWIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            790 AA;
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166
166
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243
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32.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coagulation; Kringle; Zymogen;
PLASMIN HEAVY CHAIN A.
PLASMIN LIGHT CHAIN B.
SERINE PROTEASE.
KRINGLE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X
X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 370.5; DB 1; Pred. No. 2.2e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. ..).
/FTId=CAR 000019.
O-LINKED (GALNAC. ..).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARGE RELAY SYSTEM CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KRINGLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTId=CAR_000020.
F04EA06E74BCD58E_CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 101;
                                           287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                          133
                                                                                                                                                                                                                                                                                                                                                                        580
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                                                                                                                                                                                    692
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Garriboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Havashizaki Y., Soshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=2113322, Scarman A.L., Hooper J.D., Boucaut N.J., Scarman A.L., Hooper J.D., Boucaut Normyle J.F., Antalis T.M.;
"Organization and chromosomal localization of the protease temporally expressions are in protease temporally expressions."
                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.",
Nature 409:685-690(2001).
-i- FUNCTION: COULD REGULATE PROTEOLYTIC EVENTS ASSOCIATED WITH
TESTICULAR GERM CELL MATURATION.
-i- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anch
EMBL; AF304012; AAK29360.1; -. EMBL; AY005145; AAG02255.1; -. EMBL; AF176209; AAF64407.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Testis; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteases.";
J. Biol. Che
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rothenberg M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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Mammalia; Eutheria;
                                                                                                                             or send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wong G.W., Li L., Madhusudhan M.S., Krilis S.A., Gurish M.F., Rothenberg M.E., Sali A., Stevens R.L.;
"Tryptase 4, a new member of the chromosome 17 family of mouse serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=11259427;
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28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS
CAUTION: REF.3 SEQUE
CODON IN POSITION 31
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TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL
                                                                                                                          s requires a license agreement (See http://www.an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF 3-324 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                               IN POSITION 315.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Testis;
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C 3.4.21.-) (Tryptase 4)
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HAT SHOWN
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Best Local
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PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPc; I.

PR0SITE; PS50240; TRYPSIN_DOM; I

PR0SITE; PS50134; TRYPSIN_HIS; I

PR0SITE; PS00135; TRYPSIN_SER; 1
ST14 MOUSE
P56677;
15-JUL-1999 (Re
16-OCT-2001 (Re
15-SEP-2003 (Re
Suppressor of to
ST14 OR PRSS14
                                                                            MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
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DISULFID
LIPID
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DISULFID
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CHAIN
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GO; GO:0005624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF226710; AAF64428.2; -.
EMBL; AK006271; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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InterPro; IPR001254; Ser_protease_Try.
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                                                                                                                        P 305
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                                                                                                                                                                                                                                                                              GVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGW--
                                                                                                                                                                                                                                                                                                    LRVWGNHLCGATLLNRRWVLTAAHCFOK--DNDPFDWTVOFGELTSRPSLWNLOAYSNRY
                                                                                                                                                                                                                                                                                                                          VRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQRE----GLSPGAEEV 127
                                                                                                                                                                                                                                                                                                                                                 LVVVATAAMALQSTYLQVDPEKPELQEPDLLSGPCGHRTIPSRIVGGDDAELGRWPWQGS
                                                                                                                                                                                                                          --DQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQ
                                                                                                                                                                                                                                                                                                                                                                       IVCITTYAINVSLMWLSF----RKVQEPQGKAKRHGN-TVP------
                                                                                                                                                                  GDSGGPLAC-DQDTVWYQVGVVSWGIGCGRPNRPGVYTNISHHYNWIQSTMIRNGLLRPD
                                                                                                                                                                                       GDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQS
                                                                                                                                                                                                                IGEDESLPSPNTLQEVQVAIINNSMCNHMYKKPDFR
                                                                                                                                                                                                                                                         QIEDIFLSPKYSE-QYPNDIALLKLSSPVTYNNFIQPICLLNSTYKFENRTDCWVTGWGA
                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serine protease; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                          324 AA;
          (Rel. 38, Created)
(Rel. 40, Last sequence update)
(Rel. 42, Last annotation update)
of tumorigenicity 14 (EC 3.4.21.)
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:membrane fraction;
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                                                                                                                                                                                                                                                                                                                                                                                                        11.9%;
29.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         MW;
                                                                                                                                                                                                                                                                                                                                                                                              56;
                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.

GPI-ANCHOR (POTENTIAL).

N-LINKED (GLCNAC. .) (I

N-LINKED (GLCNAC. .) (I

N-LINKED (GLCNAC. .) (I

N-LINKED (GLCNAC. .) (I

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POTENTIAL.
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(Epithin)

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RX MEDLINE=22388257; Pubbed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wapner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Wacrann K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesl
MEROPS; S01.302; -...

MGD; MG1:133881; St14.

GO; GO:0005576; C:extracellular; IDA.

GO; GO:0019897; C:extrinsic to plasma me
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; CUB-domain.
InterPro; IPR002172; LDL receptor_A.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00431; CUB; 2.
Pfam; PF00039; trypsin; 1.
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STRAIN-C.B.17SCID; TISSUE-Thymus;
MEDLINE-99216440; PubMed=10199918;
Kim M.G., Chen C., Lyu M.S., Cho E.G.,
Schwartz R.H.;
                                                                                                                                                                                                                                    EMBL; AF042822; AAD02230.3;
EMBL; BC005496; AAH05496.1;
HSSP; P20231; 1AAO.
                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformathe European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C.B.17SCID; TISSUE=Thymus;
Kim M.G., Chen C., Cho E.G., Park D., Schwartz R.H.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stromal cells encoding a new mouse typepithin, containing four LDL receptor Immunogenetics 49:420-428(1999).
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
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.17SCID; TISSUE=Thymus;
Chen C., Cho E.G., Park D.,
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Rodentia;
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SMART; SM00042; CUB; 2.
SMART; SM00192; LDLa; 4.
SMART; SM00192; LDLa; 4.
SMART; SM00192; Tryp_SPc; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01209; LDLRA_1; 2.
PROSITE; PS50068; LDLRA_2; 4.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS50240; TRYPSIN_HIS; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                           G_MOUSE
TRYG MOUSE STANDARI
OSQUET:
16-OCT-2001 (Rel. 40, 116-OCT-2001 (Rel. 40, 116-OCT-20
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CARBOTT
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ACT_SITE
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                                                                                           Tryptase gamma TPSG1 OR TMT.
                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                    Mus musculus (Mouse)
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el. 40, Last annotation updat
precursor (EC 3.4.21.-) (Tra
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                    Chordata;
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Sciurognathi; Muridae;
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                      Murinae;
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J. Biol. Chem. 274:30784-30793(1999).
                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:1349391; Tpsg1.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
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EMBL; AF175523; AAF03696.1;
HSSP; P20231; 1AAO.
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-!- TISSUE SPECIFICITY: Expressed in many tissues.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=129/SV, and BALB/c;
MEDLINE=99452974; PubMed=10521469;
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PRINTS; PR00722; CHYMOTRYPSIN.
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                                                                                                                                                                                                                                                                                          CARBOHYD
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LPAYEDWV
                                                                                            RPLCLPYPDHHLPDGERGWVLGRARPGAGIS----SLQTVPVTLLGPRACSRLHAAPGG
                                                                                                                    GSVNSSDYQVHLGELTVTLSPHFSTVKRIIMYTGSPGPPGSSGDIALVQLSSPVALSSQV
                                                                                                                                           GROAPEEWSVGLG-----TRPEEWGLKQLILHGAYTHPEGGY-DMALLLLAQPVTLGASL
                      NGSLIQPDMLCARGPGD--ACQDDSGGPLVCQVAGTWQQAGVVSWGEGCGRPDRPGVYAR
                                           DGSPILPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTA 531
                                                                      QPVCLPEASADFYPGMQCWVTGWGYTGEGEPLKPPYNLQEAKVSVVDVKTCSQAYNSP--
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Mhitning M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Botterch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
RT. Tuman and mouse cDNA sequences."
RT. Proc. Marl L. Asad Sci. U.S. A. 9016899-16601(2002)
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Suppressor of tumorisenicity 14 (EC 3.4.21.-) (Matriptase)
type serine protease 1) (MT-SP1) (Prostamin) (Serine protea
(Tumor associated differentially-expressed gene-15 protein)
ST14 OR PRSS14 OR SNC19 OR TADG15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99432178; PubMed=10500122;
Takeuchi T., Shuman M.A., Craik C.S.;
"Reverse biochemistry: Use of macromolecular procease inhibitors i dissect complex biological processes and identify a membrane-type dissect complex biological processes and normal tissue.";
serine procease in epithelial cancer and normal tissue.";
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"Molecular cloning of a novel transmembrane serine protease
" homen prografe.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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MEROPS; S01.302; ...
G0; G0:0005887; C:integral to plasma memb G0; G0:0006508; P:proteclysis and peptidd InterPro; IPR001314; Chymotrypsin.
InterPro; IPR0002172; LDL_receptor_A.
InterPro; IPR001234; Ser_protease_Try.
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Pfam; PF00089; 1dl recept a; 4.

Pfam; PF00089; trypsin; 1.

PFINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR00261; LDLRECEPTOR.

SMART; SM00042; CUB; 2.

SMART; SM00042; LDLa; 3.

SMART; SM00020; Tryp SP2; 1.

PROSITE; PS01180; CUB; 2.

PROSITE; PS01209; LDLRA 1; 2.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN HIS; 1.
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EMBL; AF133086; AAF00109.1; --
EMBL; AB030036; BAB20376.1; --
EMBL; AF057145; AAG15395.1; --
EMBL; BC005826; AAG153949.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatiche European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou
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MIM; 606797; -.
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SUBGELLULAR LOCATION: Type II membrane protein (ProbaSIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
SIMILARITY: Contains 4 LDL-receptor class A domains.
SIMILARITY: Contains 2 CUB domains.
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                SEQUENCE OF 20-10 MEDLINE=75093329; Wiman B., Wallen
                                                                                        "Characterization of a complementary human and bovine plasminogen."; Biochemistry 23:4243-4250(1984).
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Eukaryota; Metazoa;
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Structural relationship between 'glutamic

acid' and 'lysine'

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                                       CARBOHYDRATE-LINKAGE SITE SER-268
MEDLINE=97207306; PubMed=9054441;
Pirie-Shepherd S.R., Stevens R.D.
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Biol. Chem. 259:13690-13694(1984).
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76:129-137(1977).
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MEDLINE=96180681; PubMed=8611560;
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Moses M., Lane W.S., Cao Y., Sage E.H.,
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J. Mol. Biol. 212:541-552(1990).
                                       'Insertion of beta-satellite repeats
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wattenhofer M., Di Iorio V., Rabionet R., Dougherty L., Pampanos A., Schwede T., Montserrat-Sentis B., Arbones L., Iliades T., Pasquadhisceglie A., D'Amelio M., Alwan S., Rossier C., Dahl H.-H.M. Petersen M.B., Estivill X., Gasparini P., Scott H.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT DFBN8/DFNB10 GLY-103, AND VARIANTS ASN-173 MEDLINE=21904597; PubMed=11907649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rossier C., Scott H.S., Ayadi H., Guipponi M.; "Novel missense mutations of TMPRSS3 in two consanguineous Tunisian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Masmoudi S., Antonarakis S.E., Schwede T.,
Pappasavas M.P., Drira M., Elgaied-Boulila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21354482; PubMed=11462234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS
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                                                                                                 autosomal recessive neurosensory deafness 8 (DFNB8) [MIM:601072] DISEASE: Defects in TMPRSS3 are a cause of congenital autosomal recessive neurosensory deafness 10 (DFNB10) [MIM:605316]. SIMILARITY: BELONGS TO PEPFIDASE FAWILY S1. SIMILARITY: Contains 1 SRCR domain. SIMILARITY: Contains 1 LDL-receptor class A domain.
                                                                                                                                                                                                                                           IsoId=P5////--, TabG-1//;
Name=T; Synonyms=Truncated, TADG-1//;
Name=T; Synonyms=Truncated, TADG-1//;
IsoId=P57727-4; Sequence=VSP 005393, VSP 005394;
TISSUE SPECIFICITY: Expressed in many tissues inclu
Tisoform T is found at increased levels in
                                                                                                                                                                                                            DISEASE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reticulum
                                                                                                                                                                                                                                                                                                                                                                    ime=B; Synonyms=C
IsoId=P57727-2; 
                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=P57727-1;
                                                                                                                                                                                                         Undegoes autoproteolytic activation.
ASE: Defects in TMPRSS3 are a cause of childhood-onset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DFBN8/DFNB10 TRP-1
SER-111 AND VAL-253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with non-syndromic a
at. 18:101-108(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DFBN8/DFNB10 CYS-251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRP-109; PHE-194 AND
                                                                                                                                                                                                                                                                                                                                                                Sequence=VSP_005391;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             autosomal recessive
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in vitro.";
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er M.,
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PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00192; LDLa; 1.
SMART; SM00202; SR; 1.
SMART; SM00202; Tryp_SPc; 1.
PROSITE; PS001209; LDLRA 1; 1.
PROSITE; PS50068; LDLRA 2; 1.
PROSITE; PS50068; LDLRA 2; 1.
PROSITE; PS500420; SRCR 1; FALSE NEG.
PROSITE; PS50287; SRCR 2; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS502135; TRYPSIN HIS; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
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EMBL; AB038157; BAB20077.1; -
EMBL; AB038158; BAB20078.1; -
EMBL; AB038159; BAB20079.1; -
EMBL; AB038160; BAB20080.1; -
HSSP; P00763; 1DPO.
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MIM; 605511; -.
MIM; 601072; -.
MIM; 605316; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0016021; C:integral to membrane; NAS. GO; GO:0006508; P:proteclysis and peptidolysis; NAS. InterPro; IPRO01314; Chymotrypsin.

InterPro; IPR0012172; LDL_receptor_A.

InterPro; IPR001254; Ser_protease_Try.

InterPro; IPR001190; Srcr_receptor.

Pfam; PF00087; Idl recept_a; 1.

Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Serine protease; Transmembrane; Signal-anchor; Endoplasmic reticulum; Deafness; Alternative splicing;
                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                        VARSPLIC
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an email to
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SRCR.
SERINE PROTEASS.
CHARGE RELAY SYSTEM (B)
SYSMILARITY.
BY SIMILARITY.
        /FTId=VSP_005393.
Missing (In isoform 7
/FTId=VSP_005394.
                                                                                                                                                                                                                                           M-LINKED (GLCNAC. . .) (POTENTIAL).
Missing (in isoform B).
/FIId=VSP 005391.
/FIId=VSP 005391.
EMIQPVCLPNSEENFPDGKVCWTSGWGATEDGAGDASPVLN
EMIQPVCLFNSEENFPDGKVCWTSGWGATEDGAGDASPVLN
HAAVPLLSNKICNHRDVYGGIISPSMLCAGYLTGGVDSCGG
DSGGPLVCOERRLUKKLVGATSFGIGCAEVNKPGVYTRVTSG
DSGGPLVCOERRLUKKLVGATSFGIGCAEVNKPGVYTRVTSG
DSGGPLVCOERRLUKKLVGATSFGIGCAEVNKPGVTRVTSG
DSGGPLVCOERRLUKT -> GTSGSLCGSAALPLFQEDLQLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITUPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE (POTENTIAL).
EXTRACET TO THE STATE ACTION OF THE 
                                                                                                                                EAFL (in isoform D).
/FIId=VSP_005392.
DLYLDKSWTIOVGLVSLLDNPAPSHLVEKIVYH
PRERADRRGRKLLCWRKPTKMKGPRPSHS (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
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ר מא	109 111 173 194 251 253 253 404 407	103
/F  46  54  /F  /K  II.6%; Sc  33.1%; pr ; Conservative 39;  CVACGSLRTAGPQAGAP	109 111 173 194 251 253 407	103
10 G_G_G_G_E_S_S_S_S_S_S_S_S_S_S_S_S_S_S_S_	R -> W (in DFNB8/DFNB10)	/FTId=VAR_010781. D -> G (in DFNB8/DFNB10). /FTId=VAR_013490.

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2: sp_bacteria:*

3: sp_fungi:*
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   GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd
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                                         1524
331
802
811
339
340
317
                                                                                                                                                                                                                      DB
                                                   Q8R1A6
Q8IUE2
Q8IU80
Q99L44
Q8BJV6
                                                                                                                  Q8NF86
Q91674
                                                                                                                                          Q8CFX9
Q8NBY4
Q8BJR6
L Q8BJR6
L Q9DBIO
                                                                                                                                                                                                                      ij
 Q9DGR3
O88781
Q90WD8
P79953
                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               830525
OBCEX9 mus musculu
OBnby4 homo sapien
OBbjr6 mus musculu
O9dbi0 mus musculu
O9dbi0 mus musculu
O9dbi71 homo sapien
OBnf86 homo sapien
O8nf86 homo sapien
O8nf86 homo sapien
O91674 xenopus lae
O81424 komo sapien
O8iue2 homo sapien
O8iue2 homo sapien
O8iue3 homo sapien
O9144 mus musculu
O8bjv6 mus musculu
O8bjv6 mus musculu
O9dgr3 xenopus lae
O88781 rattus ratt
O90wd8 bufo japoni
P79953 xenopus lae
                                                                                                                                                                                                                      Description
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	<b>4</b> 5	44	43	42	41	40	39	38	37	36	ω G	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
		w	339	340.5			342.5	343	343	343	344	4	347.5	348.5	349	349.5	351	56	356.5	60	361.5	364	64	368.5	69	71	75	378	
		0					11.0												11.5					11.9		12.0		12.2	
	490	471	310	624	537	322	282	806	624	3 3 5	667	581	455	453	624	453	454	445	371	810	422	423	334	855	329	812	812	389	321
	11	11	1	φ	4	1	1	σ	11	11	ហ	4	11	11	11	11	თ	11	11	4	4	11	σ	11	13	11	1	13	4.
1	Q920K3	Q8CFE0	Q91XC4	Q95ME7	Q9BYE1	Q920S2	Q9D4I3	018783	Q91Y47	Q8VIF2	Q9BJM1	Q9BYE2	Q8CDR0	Q8K1T0	Q9DAT3	Q8VDE0	046506	Q8CJ17	Q8CJ16	Q15146	Q8WVC1	QBBM10	046507	Q9JJI7	042272	Q91WJ5	Q9R0W3	Q9PVX7	Q96RZ8
	ratt	Q8cfe0 mus musculu	Q91xc4 mus musculu	oryc	Q9byel homo sapien	mus	Q9d4i3 mus musculu	O18783 macropus eu	. Q91y47 mus musculu	Q8vif2 mus musculu	trich	Q9bye2 homo sapien	Q8cdr0 mus musculu	Q8k1t0 mus musculu	Q9dat3 mus musculu	Q8vde0 mus musculu	O46506 papio hamad	Q8cj17 rattus norv	Q8cj16 rattus norv	OMO	homo	Q8bm10 mus musculu	O46507 papio hamad	Q9jji7 rattus norv	O42272 xenopus lae	Q91wj5 mus musculu	Q9r0w3 rattus norv	Q9pvx7 xenopus lae	Q96rz8 homo sapien

## ALIGNMENTS

Ş	Db	δδ	Дb	δ	뫄	δ		SQ	T 2	R R	RC	R P	2 0	8	86		DI C	348	ם ב	RE Q8
328 SPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLI 387	124 AQEDTPVLLTDMAVHSSWLQAHVHEAAFLVQAPGVVKMSDENSCVACGSLRSAGPQAGAL 183	268 AQEDAPVLITNTAAHSSWLQARVQGAAFLAQSPETPEMSDEDSCVACGSLRTAGPQAGAP 327	64 LYNRLHQRLLSNPARPGMLCGGAQPGEQGPCQGDSGGPVMCREPDGHWVQVGIISFTSKC 123	208 IY	4 ALLQLTHPTVQTTLCLPQPTYHPPFGASCWATGWDQNTSDVSRTLRNLRLRLISRPTCNC 63	148 ALLQLAHPTTHTPLCLPQPAHREPFGASCWATGWDQDTSDAPGTLRNLRLRLISRPTCNC 207	Query Match 60.1%; Score 1868.5; DB 11; Length 426; Best Local Similarity 80.0%; Pred. No. 2.3e-131; Matches 339; Conservative 21; Mismatches 63; Indels 1; Gaps 1;	SEQUENCE 426 AA; 4	NON TER 1 1		STRAIN-FVB/N;	SEQUENCE FROM N.A.		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Similar to pr	01-MAR-2003 (TrEMBLrel. 23, L	01-MAR-2003 (TrEMBLrel. 23, Creat		RESULT 1 QBCFX9

360

548

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                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Sim
Matches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBNBY4;
01-OCT-2002 (TrEMBLrel. 22, Crea
01-OCT-2002 (TrEMBLrel. 22, Last
01-MAR-2003 (TrEMBLrel. 23, Last
Hypothetical protein FLJ90661.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00089; trypsin; 3.

PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp SPC; 3.

PROSITE; PS50240; TRYPSIN DOM; 3.

PROSITE; PS00135; TRYPSIN SER; 1.

Hypothetical protein; Hydrolase; Protease; Serin SEQUENCE 766 AA; 82564 MW; 3630D550CB06BD55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE, Placenta;
Igogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama 'Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Suzuki Y., Nagai K., Sugano S., Ishii S., Kojima S., Nagahari K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8NBY4
         191
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                                                                                                                                                                                                                                                                                     12
                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                            PARPGMLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNT
                                                                                                                                                                                                                     PQPAHRFPFGASCWATGW----DQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OSTG
    ATYEAWIREQVMGSEPGPAFPTQPQKTQSDPQEPREENCTIALPECG------KAPRPG
                                               AAHSSWLQARVQGA----AFLAQSPET---PEMSDEDSCV----ACGSLRTAGPQAGAPS 328
                                                                                          QILPGMLCAGYPEGRRDTCQGDSGGPLVC-EEGGRWFQAGITSFGFGCGRRNRPGVFTAV
                                                                                                                                                                                                                                                                                                                         WSVVLGSLQREGLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTT----HTPLCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WFLAGLHSFGDACQGPARPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEPGSCLANISQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YPQTVPVTVLGPMACSRQHAAPGGTGIPILPGMVCTTVVGEPPHCEGLSGAPLVHEIRGT
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                                                                                                                                                                                     PRASHREVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFNLTL
                                                                                                                                                                                                                                                                                WSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WFLVGLHSFGDTCQSSAKPAVFAALSAYEDWISNLDWQVYFAEEPEPEAETGSCLVNSSQ
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                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                       Score 724; DB 4; Length 766; Pred. No. 1.1e-45; Mismatches 189; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       766
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6BD55 CRC64;
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OBBJR6
ID BG
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Q9DBI0
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the RIKEN Genome Exploration Research Group Phase I & II Team; Phalysis of the mouse transcriptome based on functional annotation 60,770 full-length CDNAs.";
Nature 420:563-573 (2002).
EMBL; AK080281; BAC37864.1; -.
SEQUENCE 328 AA; 35789 MW; DC0B20F1AB3EB840 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel 23, Created)
01-MAR-2003 (TrEMBLrel 23, Last sequence up
01-MAR-2003 (TrEMBLrel 23, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8BJR6;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similar to MARAPSIN precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 NTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 15.5%; Score 481.5; DB
Similarity 36.1%; Pred. No. 5e-28;
99; Conservative 46; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NALEGEWPWQVSIQRNGIHFCGGSLIAPTWVLTAAHCFSN--TSDISIYQVLLGALKLQQ 100
                                                                                                                                                                                                                QPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARV
                                                                                                                                                                                                                                                                                                                                                                       PGPHALYVPVKQVKSNPQYQGMASSADVALVELQGPVTFTNYILPVCLPDPSVIFESGMN
                                                                                          PELQFQGRAGTQQQQKDSQ-----GQQRLAGNSA 308
                                                                                                                                                                                                                                                                              CWVTGWGSPSEQDRLPNPRVLQKLAVPIIDTPKCNLLYNKDVESDFQLKTIKDDMLCAGF
                                                                                                                                      QGAAFLAQSPETPEMSDEDSCVACGSLRTAGPQA 324
                                                                                                                                                                                   AEGKKDACKGDSGGPLVCL-VDQSWVQAGVISWGEGCARRNRPGVYIRVTSHHKWIHQII
                                                                                                                                                                                                                                                                                                                         CWATGW----DQDTSDAPGTLRNLRLISRPTCNCIYNQ-LHQRHLSNPARPGMLCGGP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAWDWGPDGEETETQTCPPHTEHGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVARLVQHENASW-DNASDLALLQLRTPVNLSAASRPVCLPHPEHYFLPGSRCRLARW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLKQLTLHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGER----GWVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AWPWEAQVMVPGSRPCHGALVSESWVLAPASCFLDPNSSDSPPRDLDAWRVLLPSRPRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CWNDSRWSLLCQEEGTWFLAGIRDFPSGC---LRPRAFFPLQTHGPWISHVTRGAYLEDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVSSLDWQVYF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRGEPALGPGAL--LEAELLGGWWCHCLYGRQGAAVPLPGDP--PHALCPAYQEKEEVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRARPGAGISSLQTVPVTLLGPRACSRLHAAPGG----DGSPILPGMVCTS--AVGELPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEE-----WSVGLGTRPEEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----AEEPE----PEAEPGSC 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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DB 11; Length

328; 17;

Of

112; Indels

Gaps

220

8

update)

update)

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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Pukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schai K., Okido T., Furuno M., Aono H., Baldar, dle Bonaldo M.F.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldar, dle Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., Geniboldi M.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaetts P.,
RA Ovrdone P., Ring B., Ringwald M., Mazzarelli J., Mombaetts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Mynshaw-Boris R., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
                       S
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                                                                                                                                    Matches
                                                                                                                                                                     Query Match
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MGD; MGI:1919003; Tmpras6.

InterPro; IPR001314; Chymotrypsin.

InterPro; IPR001314; Chymotrypsin.

InterPro; IPR001254; Ser_protease_Try.

InterPro; IPR001254; CHYMOTRYPSIN.

PRINTS; PR00172; CHYMOTRYPSIN.

PRINTS; PR00126; LDLRA_1; 1.

PROSITE; PS01180; CUB; 1.

PROSITE; PS01180; CUB; 1.

PROSITE; PS01209; LDLRA_1; 1.

PROSITE; PS0134; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence upd
01-MAR-2003 (TrEMBLrel. 23, Last annotation u
130008A22Rik protein (RIKEN cDNA 1300008A22
TMPRSS6 OR 1300008A22RIK.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausherg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; AK004939; BAB23684.1; -.
EMBL; BC029645; AAH29645.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=Liver; MEDLINE=21085660; PubMed=11217851; Kawai J., Shinagawa A., Shibata K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashizaki Y
                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001).
                                                                                                                                                     Local
                                                             559
                        109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P00763; 1DPO.
                                                                                                                                                     Similarity
SVVLGSLQREGLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT-----
                                                                            QGKÄKR-HGNTV--PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSW
                                                       QGLSSRIVGGTVSSEGEWPWQASLQIRGRHICGGALIADRWVITAAHCFQEDSMASPKLW
                                                                                                                                    Conservative
                                                                                                                                                                                                         ΑA;
                                                                                                                                                                                                 89557 MW;
                                                                                                                                                   14.5%;
37.6%;
                                                                                                                                  40;
                                                                                                                              Score 451.5; DB 1
Pred. No. 2.5e-25;
0; Mismatches 96
                                                                                                                                                                                                         16315A646A4D5288 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         799
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                                                                                                                                                                     DB 11;
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2 gene).
                                                                                                                                96;
                                                                                                                                  Indels
                                                                                                                                                                   Length
                                                                                                                                  17;
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                                                                                                                              Gaps
 - PLCLP
                                                           819
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Query Match
Best Local
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NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; BC036846; AAH36846.1; -.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_Spc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similar to protease, serine, 8 (Prostasin) (Fragment). Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8N171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8N171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                791
  322
                                                                                      263
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                                                                                                                                                                                                                                                                             151
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                                             287
                                                                                                                                 227
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                                                                                                                                                                                                                                                                                                                                                                        93
                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                GEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPG 123
                                                                                                                                                                                                                                                                                                                        AEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INWIQ 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QPAHREPEGASCWATGWDQDTSDAP--GTLRNLRLRLISRETCNCIYNQLHQRHLSNEAR 222
QARV 325
                                                                                                                                                                                                                                                                          TLSVPVRRVLLPPDYSEDGARGDLALLQLRRPVPLSARVQPVCLPVPGARPPPGTPCRVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSWLQ 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRMLCAGYRKGKKDACQGDSGGPLVCREPSGRWFLAGLVSWGLGCGRPNFFGVYTRVTRV 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGMLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARSHFFEPGQHCWITGWGAQREGGPVSNTLQKVDVQLVPQDLCSEAYRY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVFLGKMRQNSRWPGEVSFKVSRLFLHPYHEEDSHDYDVALLQLDHPVVYSATVRPVCLP 678
                                                                                                                                                                                                                                                                                                                                                                      GEWPWQASIQHRGAHVCGGSLIAPQWVLTAAHCFPRRALPA--EYRVRLGALRLGSTSPR
                                             QARV
                                                                                        CAGYPQGHKDACQGDSGGPLTCLQ-SGSWVLVGVVSWGKGCALPNRPGVYTSVATYSPWI
                                                                                                                                 CGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWL 286
                                                                                                                                                                                 GWG--
                                                                                                                                                                                                                             GWDQDTSDAPGT-----LRNLRLRLISRPTCNCIYN-----QLHQRHLSNPARPGML 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327 AA; 35106 MW; 60458ED817AC1CF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                               -SLRPGVPLPEWRPLQGVRVPLLDSRTCDGLYHVGADVPQAERIVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.4%; Score 448; DB 4; Le 41.0%; Pred. No. 1.6e-25; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Best Local Sin
Matches 101;
[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=99432219; PubMed=10500163;
Lindsay L.L., Yang J.C., Hedrick J.L.;
Lindsay L.L., Yang J.C., Hedrick J.L.;
"Ovochymase, a Xenopus laevis egg extracellular protease,"
"Ovochymase, a Xenopus laevis egg extracellular protease,"
translated as part of an unusual polyprotease.";
translated as part of an unusual polyprotease.";
                                                                                                                                                                                                                                                                                                                                                                                                                     Q91674;
Q91674;
01-NOV-1996
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01-OCT-2002
01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO PEPTIDASE F
EMBL; AF536382; AAN04055.1; -.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine protease EOS
                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vej
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase;
SEQUENCE
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                                                                                                                                                                                                                    NCBI_TaxID=8355;
                                                                                                                                                                                                                                                   Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                 Polyprotein.
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40.7%; Pred. No. 1.60
tive 31; Mismatches
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N; FDF3F1750D569978 CRC64;
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                                                     WQVQIFFLRTFHCEGAIISPQWILTAAHC-IRAAEPSYWTVIAGDHNRMLNESTEQIRNI
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SMART; SM00042; CUB; 4.

SMART; SM00020; Tryp_SPc; 3.

PROSITE; PS001180; CUB; 5.

PROSITE; PS50240; TRYPSIN_DOM; 3.

PROSITE; PS00134; TRYPSIN_HIS; 3.

PROSITE; PS00135; TRYPSIN_SER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "CDNA Cloning of Ovochymase, a Chymotrypsin-like Protease From Xenopus laevis Eggs at Fertilization."; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: CONTAINS 4 CUB DOMAINS.
EMBL; U81290; AAC24717.1; -.
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InterPro; IPR001859; CUB domain.
InterPro; IPR001254; Ser_protease_;
Pfam; PF00431; CUB; 5.
Pfam; PF00089; trypsin; 3.
PFINTS; PR00722; CHYMOTRYPSIN.
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SEQUENCE FROM N.A.
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HSSP; P00763;
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147; Conserv
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WEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEEWSVGLG-----TRPEEWGL
                                       KFSFVPKEKQFSLPVDDTPTISMLHPRAIALDVCGMAPMTPKWWLPRIVGGEEASPNSWP
                                                                                                                    VEYGHGCIYDAVEVYDGABEKQLIARLCGYTLPLPISSPENTMLIRFKTDMENSYPGFKV
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SERINE PROTEASE
OVOCHYMASE.
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Pred. No. 4.9
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SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN SER; 1.

PROSITE; PS00135; TRYPSIN SER; 1.
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Q8R1A6;
01-JUN-2002
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01-MAR-2003 (TrEMBLrel. 21,
01-MAR-2003 (TrEMBLrel. 23,
RIKEN CDNA 2010001P08 gene.
2010001P08RTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2002) to the EMBL; BC024903; AAH24903.1; HSSP; P00761; 1AN1.
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Mus musculus (Mouse).
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                                                                                                                                HLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVL
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YTNVSVYISWIQNTMWNLPMEGRGFSPSLSGTP 314
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; Pred. No. 1.2e-24;
47; Mismatches 102;
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W; C06F6EF2FA261636 CRC64;
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Q8IUE2;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                              QBIU80;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Dast annotation update)
                                                 SEQUENCE FROM N.A.
HOODER J.D., Quigley J.P.;
"TMPRSS6, a new type II transmembrane serine protease.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY055383; AALL6413.1; -.
EMBL; AY055384; AALL6414.1; -.
Protease; Transmembrane.
SEQUENCE 811 AA; 89999 MW; 7EEF193F655DDE9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22241917; PubMed=12149247;
Velasco G., Cal S., Quesada V., Sanchez L.M., Lopez-Otin C.;
"Matriptase-2, a membrane-bound mosaic serine proteinase predominantly expressed in human liver and showing degrading activity against extracellular matrix proteins.";
J. Biol. Chem. 277:37637-37646(2002).
EMBL; AJ319876; CAC85953.1; -.
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                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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87; Conservative
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9; Mismatches
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                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Matches 87; Conservative
  Query Match
                                                                                                    InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser protease Try.
Pfam; PP00089; trypsin; 1
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS00134; TRYPSIN DDM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
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Q99L44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kitamura K., Takefumi N., Kimio T.;
"mouse serine protease.";
Submitted (PEB-2000) to the EMBL/GenBank/DDBJ databases
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Mus musculus (Mouse).
Mus musculus (Mouse).
Mus musculus (Mouse).
Merazoa; Chordata;
Merazoa; Rodentia;
                                                        Hydrolase;
SEQUENCE
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Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                               MGD; MGI:1923810; Prss8.
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                                                                                 Protease;
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9; Mismatches 106
  Score
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Best Local S
Matches 92
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The FAMTOM Consortium,
The RIKEN Genome Exploration Research G
"Analysis of the mouse transcriptome ba
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
LEMBL; AK078696; BAC37362.1; -
2 EMBL; AK078696; BAC37362.1; -
340 AA; 36503 MW; 3C2540E
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Q8BJV6;
Q1-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Eye;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       GAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGQWPWQVSITYDGNHVCGGSLVSNKWVVSAAHCFPREHSRE--AYEVKLGDHQLDSYSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSAKPGQWPWQVSITYDGNHVCGGSLVSNKWVVSAAHCFPREHSRE--AYEVKLGAHQLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQRE
                                                                                                          ARVQGAAFLAQSPETPE 304
                                                                                                                                                                                                                    QGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSW------LQ
                                                                                                                                                                                                                                                                                                                            TGW----DQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGV
                                                                                                                                                                                                                                                                                                                                                                                 DTVVHTVAQIITHSSYREEGSQGDIALIRLSSPVTFSRYIRPICLPAANASFPNGLHCTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AELQPRV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --LOARVOGAAFLAOSPETPE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKGGKDACQGDSGGPLSC-PMEGIWYLAGIVSWGDACGAPNRPGVYTLTSTYASWIHHHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HCTVTGWGHVAPSVSLQTPRPLQQLEVPLISRETCSCLYNINAVPEEPHTIQQDMLCAGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCWATGW----DQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSNDTVVHTVAQIITHSSYREEGSQGDIALIRLSSPVTFSRYIRPICLPAANASFPNGL
                                                                                                                                                                  KDACQGDSGGPLSC-PMEGIWYLAGIVSWGDACGAPNRPGVYTLTSTYASWIHHHVAELQ
                                                                                                                                                                                                                                                                          TGWGHVAPSVSLQTPRPLQQLEVPLISRETCSCLYNINAVPEEPHTIQQDMLCAGYVKGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exploration Research Group Phase I & II mouse transcriptome based on functional
                                                        -- VPQTQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.3%;
35.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----VPQTQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41;
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Last sequ
Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 412; DB 11;
Pred. No. 7.9e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 2.8e-23;
L; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3C2540E9B3A81C8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340;
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Gaps

122

234

287 231

290

178

111

171

of.

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RESULT 14
00878
ID 00878
AC 08878
AC 08878
DT 01-NC
DT 01-MA
CDT 01-MA
GN SETIN
GN BSP2
OS RATEU
OC EUKAZ
OC Mamma
OC NCBI
RP SEQUE
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Q9DGR3
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Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                        O88781;
01-NOV-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00089; trypsin; 1.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Protease; Serine protea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                         Serine
BSP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9DGR3;
01-MAR-2001
                        Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10117;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from Xenopus laevis.";
Gene 252:209-216(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Embryonic serine protease-1
                                                                                                                 Rattus rattus (Black rat)
                                                                                                                                                                                       01-MAR-2003
                                                                                                                                                                                                                                                                                   088781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB038496; BAB08216.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20363741; PubMed=10903452;
Yamada K., Takabatake T., Takeshima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XESP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9DGR3
  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001254; Ser_protease_Try.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kenopodinae; Kenopus
                                                                                                                                                                                                                                                                                                                                                                                                     277
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                                                                                                                                                             protease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREG
  FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CWATGWDQDTSDA----PGTLRNLRLRLISRPTCNCIYNQLHQRHLSNP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KNPHEMTVKVDIIYINSEFNGPGTSGDIALLKLSSPIKFTEYILPICLPASPVTFSSGTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPPFGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DTRQGAWPWQVSLEFNGSHICGGSIISDQWILTATHCIEHPDLP--SGCGVRLGAYQLYV
                                                                                                                                                                                                                                                                                                                                                                                                  WISER----SVISFKPFTSSSSPSSSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                              WLQARVQGAAFLAQSPETPEMSDEDSCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QICAGY
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                                                                                                                                                        3 (TrEMBLrel. 08, 08 (TrEMBLrel. 08, 13 (TrEMBLrel. 23, 14 (TremBLrel. 23, 15 (TremBLrel. 23))
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                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QAGQKDGCQGDSGGPLVC-KIQGFWYQAGIVSWGERCAAKNRPGVYTFVPAYET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34413 MW;
                                                                   Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.0%;
                                                                                                                                                             (Fragment)
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Last annotation updat
                                                                                                                                                                              Last sequence update)
Last annotation updat
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Pred. No. 2.4e-
45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protease
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                                                                                                                                                                                                                                Created)
                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEC78A9F46D138FE
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                                                                                                                                                                                  update)
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                                                                   Rattus
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RESULT 15
Q90WD
AC Q90WD
AC Q90WD
AC Q90WD
DT 01-DE
DT 01-DE
DT 01-MA
DE Ovidu
OS Bufo
OC Eukax
OC Amphi
OX NCBI
RN [1]
RN [1]
RN [1]
RP SEQUE
RA Hiyos
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                             01-DEC-2001
01-DEC-2001
01-MAR-2003
                   MBL/GenBa DMAINS, ABLONGS TO PEPTIDASE E.

MBL; AB070367; BAB63372.1; --

MEROPS; P00761; IANI.

MEROPS; S01.240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                   TISSUB-oviductal pars recta;
Hiyoshi M., Takamune K., Mita K., Kubo H., Sugimoto Y., K
"Oviductal, the oviductal protease that mediates gamete i
affecting the vitelline envelope in Bufo japonicus: Its m
cloning and analyses of expression and post-translational
                                                                                                                                                                                                                                              Bufo japonicus (Japanese toad).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae; I
NCBI_TaxID=8387;
                                                                                                                                                                                                                                                                                                                                                                              Q90WD8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001254; Ser protease_Try.
Pfam; PF00089; trypsin; 1.
SMART; SM00020; Tryp_SPC; 1.
SROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                          activation.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI--i- SIMILARITY: CONTAINS 2 CUB DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Protease; Serine protease; NON TER 1 1 1 POTENTIAL <1 23 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Davies B.J., Pickard B.S., Steel M., Morris R.G., "Serine Proteases in Rodent Hippocampus.";
J. Biol. Chem. 273:23004-23011(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Fisher; TISSUE=Brain;
MEDLINE=98389725; PubMed=9722524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; S01.
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
              nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         277
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; S01.240; -.
ro; IPR001314;
ro; IPR000859;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKAKRHGNTVPGE------WPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GQEAITEDMLCAGYLEGKRDACLGDSGGPLMC-QVDDHWLLTGIISWGEGCAERNRPGVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLPQPAHRFPFGASCWATGW----DQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWSVVLGSLQREGLSPGAEEVGVAA-LQLPRAYNHYSQGSDLALLQLAHPTTHT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKPQQLNRVVGGEDSADAQWPWIVSILKNGSHHCAGSLLTNRWVVSAAHCF-SSNMDKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYSVLLGAWKLGNPGPRSQKVGIASVLPHPRYSRKEGTHADIALVRLERPIQFSERILPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSLLAHRPWVQRIVQGVQLRGRLADSGDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNTAAHSSWLQARVQGAAF---LAQSPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNPA-RPGMLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLPDSSVHLPPNTNCWIAGWGSIQDGVPLPRPQTLQKLKVPIIDPELCKSLY----WRGA
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24
297 AA;
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 Chymotrypsin CUB_domain.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                              Created)
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Pred. No. 8.2e-22;
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                                                                                                                                                                        interaction
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Best Local Similarity 19.5
Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00042; CUB; 2.

SMART; SM000020; TTYD_SC; 2.

PROSITE; PS01180; CUB; 2.

PROSITE; PS50240; TRYPSIN_DOM; 2.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

Hydrolase; Protease; Serine protease.

SEQUENCE 974 AA; 107647 MW; F19705A470465553 CRC64;
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Pfam; PF000431; CUB; 2.
Pfam; PF00089; trypsin; 2.
PF10175; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                           376 TRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGE---
                                                                                                                                                                                                                                                                                                                                                                                 599 NGWPWHVSINFGNKHVCNGAILSKTFVVTSANCVADREEFPSIGLIVAGLHDLESSINTQ 658
                                              490 PSCEGLSGAPLV-HEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWV 539
                                                                                                                      715 VSGWDLNVELS----TKLQQLEVPVLMDDVCKKYY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 - CORSOGRWYLVGVTSWGLGCARKWADNILDPVESKGSPGVFTDIQRLLNWLSENLNQDK 302
764 ASCLAQSGAPLVCQSAPGTYAIFGIVSRGVGCNETPKAGVYSSVFLFIPWI 814
                                                                                                                                                                                     433 -RGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTSAVGE--L 489
                                                                                                                                                                                                                                                   659 KRPVEY----VÍVHPDÝNRLSKDÝDVÁLIHVQRPFQYNSYVQPIČLPDGHSRLEPSKLCV 714
                                                                                                                                                                                                                                                                                                                                                                                                                                            328 SPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQA-PE-----EWSVGLG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           543 VISFVLPSSPVKPEKGNNQPRKNQDAMQHFDEGCG----VSPLPPRFLYHNLIKAEEAMP 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 -----LAQSPETPE-----MSDEDSC----VACGSLRTAGP-------QAGAP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     483 VEPSEGCIFDRLVVYHDLQGTVVAGFFCGFALPDPVLSVSNVMQITFTSDYSANYLGFRA 542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 LCLEPDGHWVQAGIISFASSCAQ-----EDA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 RLPSSLQKVVLPLIEYRRCLSİMETVDRR----LAFETVVCAĞFPEĞGKDACQĞDSĞĞPF 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 DAPGTIRNIRIRISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 KPSRPFNY-----DLAILELVESITFDKDIQPACLPSPDDVFPTGTLCMALGWGRLQENG 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 ISDKYVLTAAHCVLEKNFEFQVSVSIGDHDFAVYERSEQRFAIK------SVFKHPNF 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 RGVTDSPGRVSRCGERPAANTSVSYGLLSRIVGGTSAVKGESPWMVSLKRDGKHFCGGTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.7%; Score 394.5; DB 13; Length 974;
19.5%; Pred. No. 5.5e-21;
vative 83; Mismatches 213; Indels 373;
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                                                                                                                         -DG--ITDRMFCAGVIAEEDN 763
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Search completed: January 6, 2004, 10:02:38 Job time : 43 secs